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ATTENTION: APPLICATION BRANCH

Sir:

Transmitted herewith for filing is the patent application of

Inventor(s): Jean-Baptiste Dumas Milne Edwards, Aymeric Duclert, and Lydie Bougueleret

For: EXTENDED cDNAs FOR SECRETED PROTEINS

Enclosed are:

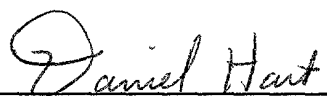
- (X) Sixteen (16) sheet(s) of informal drawings.
- (X) Sequence Listing in 220 pages.
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CLAIMS AS FILED

FOR	NUMBER FILED	NUMBER EXTRA	RATE	FEE
Basic Fee			\$760	\$760
Total Claims	18 - 20 =	0 x	\$18	\$0
Independent Claims	15 - 3 =	12 x	\$78	\$936
If application contains any multiple dependent claims(s), then add			\$270	\$0
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EXTENDED cDNAs FOR SECRETED PROTEINS

Related U.S. Application Data

The present application claims priority from United States Provisional Application Serial No:
5 60/066,677, filed November 13, 1997, the entirety of which is hereby incorporated by reference.

Background of the Invention

The estimated 50,000-100,000 genes scattered along the human chromosomes offer tremendous
promise for the understanding, diagnosis, and treatment of human diseases. In addition, probes capable of
10 specifically hybridizing to loci distributed throughout the human genome find applications in the
construction of high resolution chromosome maps and in the identification of individuals.

In the past, the characterization of even a single human gene was a painstaking process, requiring
years of effort. Recent developments in the areas of cloning vectors, DNA sequencing, and computer
technology have merged to greatly accelerate the rate at which human genes can be isolated, sequenced,
15 mapped, and characterized. Cloning vectors such as yeast artificial chromosomes (YACs) and bacterial
artificial chromosomes (BACs) are able to accept DNA inserts ranging from 300 to 1000 kilobases (kb) or
100-400 kb in length respectively, thereby facilitating the manipulation and ordering of DNA sequences
distributed over great distances on the human chromosomes. Automated DNA sequencing machines permit
the rapid sequencing of human genes. Bioinformatics software enables the comparison of nucleic acid and
20 protein sequences, thereby assisting in the characterization of human gene products.

Currently, two different approaches are being pursued for identifying and characterizing the genes
distributed along the human genome. In one approach, large fragments of genomic DNA are isolated,
cloned, and sequenced. Potential open reading frames in these genomic sequences are identified using bio-
informatics software. However, this approach entails sequencing large stretches of human DNA which do
not encode proteins in order to find the protein encoding sequences scattered throughout the genome. In
25 addition to requiring extensive sequencing, the bio-informatics software may mischaracterize the genomic
sequences obtained. Thus, the software may produce false positives in which non-coding DNA is
mischaracterized as coding DNA or false negatives in which coding DNA is mislabeled as non-coding
DNA.

An alternative approach takes a more direct route to identifying and characterizing human genes.
30 In this approach, complementary DNAs (cDNAs) are synthesized from isolated messenger RNAs (mRNAs)
which encode human proteins. Using this approach, sequencing is only performed on DNA which is
derived from protein coding portions of the genome. Often, only short stretches of the cDNAs are
sequenced to obtain sequences called expressed sequence tags (ESTs). The ESTs may then be used to
35 isolate or purify extended cDNAs which include sequences adjacent to the EST sequences. The extended
cDNAs may contain all of the sequence of the EST which was used to obtain them or only a portion of the
sequence of the EST which was used to obtain them. In addition, the extended cDNAs may contain the full

coding sequence of the gene from which the EST was derived or, alternatively, the extended cDNAs may include portions of the coding sequence of the gene from which the EST was derived. It will be appreciated that there may be several extended cDNAs which include the EST sequence as a result of alternate splicing or the activity of alternative promoters.

5 In the past, the short EST sequences which could be used to isolate or purify extended cDNAs were often obtained from oligo-dT primed cDNA libraries. Accordingly, they mainly corresponded to the 3' untranslated region of the mRNA. In part, the prevalence of EST sequences derived from the 3' end of the mRNA is a result of the fact that typical techniques for obtaining cDNAs, are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs. (Adams et al., *Nature* **377**:174, 1996, Hillier et al.,
10 *Genome Res.* **6**:807-828, 1996).

In addition, in those reported instances where longer cDNA sequences have been obtained, the reported sequences typically correspond to coding sequences and do not include the full 5' untranslated region of the mRNA from which the cDNA is derived. Such incomplete sequences may not include the first exon of the mRNA, particularly in situations where the first exon is short. Furthermore, they may not
15 include some exons, often short ones, which are located upstream of splicing sites. Thus, there is a need to obtain sequences derived from the 5' ends of mRNAs which can be used to obtain extended cDNAs which may include the 5' sequences contained in the 5' ESTs.

While many sequences derived from human chromosomes have practical applications, approaches based on the identification and characterization of those chromosomal sequences which encode a protein product are particularly relevant to diagnostic and therapeutic uses. Of the 50,000-100,000 protein coding
20 genes, those genes encoding proteins which are secreted from the cell in which they are synthesized, as well as the secreted proteins themselves, are particularly valuable as potential therapeutic agents. Such proteins are often involved in cell to cell communication and may be responsible for producing a clinically relevant response in their target cells.

25 In fact, several secretory proteins, including tissue plasminogen activator, G-CSF, GM-CSF, erythropoietin, human growth hormone, insulin, interferon- α , interferon- β , interferon- γ , and interleukin-2, are currently in clinical use. These proteins are used to treat a wide range of conditions, including acute myocardial infarction, acute ischemic stroke, anemia, diabetes, growth hormone deficiency, hepatitis, kidney carcinoma, chemotherapy induced neutropenia and multiple sclerosis. For these reasons, extended
30 cDNAs encoding secreted proteins or portions thereof represent a particularly valuable source of therapeutic agents. Thus, there is a need for the identification and characterization of secreted proteins and the nucleic acids encoding them.

In addition to being therapeutically useful themselves, secretory proteins include short peptides, called signal peptides, at their amino termini which direct their secretion. These signal peptides are encoded
35 by the signal sequences located at the 5' ends of the coding sequences of genes encoding secreted proteins. Because these signal peptides will direct the extracellular secretion of any protein to which they are

operably linked, the signal sequences may be exploited to direct the efficient secretion of any protein by operably linking the signal sequences to a gene encoding the protein for which secretion is desired. This may prove beneficial in gene therapy strategies in which it is desired to deliver a particular gene product to cells other than the cell in which it is produced. Signal sequences encoding signal peptides also find application in simplifying protein purification techniques. In such applications, the extracellular secretion of the desired protein greatly facilitates purification by reducing the number of undesired proteins from which the desired protein must be selected. Thus, there exists a need to identify and characterize the 5' portions of the genes for secretory proteins which encode signal peptides.

Public information on the number of human genes for which the promoters and upstream regulatory regions have been identified and characterized is quite limited. In part, this may be due to the difficulty of isolating such regulatory sequences. Upstream regulatory sequences such as transcription factor binding sites are typically too short to be utilized as probes for isolating promoters from human genomic libraries. Recently, some approaches have been developed to isolate human promoters. One of them consists of making a CpG island library (Cross, S.H. et al., Purification of CpG Islands using a Methylated DNA Binding Column, *Nature Genetics* 6: 236-244 (1994)). The second consists of isolating human genomic DNA sequences containing SpeI binding sites by the use of SpeI binding protein. (Mortlock et al., *Genome Res.* 6:327-335, 1996). Both of these approaches have their limits due to a lack of specificity or of comprehensiveness.

5' ESTs and extended cDNAs obtainable therefrom may be used to efficiently identify and isolate upstream regulatory regions which control the location, developmental stage, rate, and quantity of protein synthesis, as well as the stability of the mRNA. Theil et al., *BioFactors* 4:87-93 (1993). Once identified and characterized, these regulatory regions may be utilized in gene therapy or protein purification schemes to obtain the desired amount and locations of protein synthesis or to inhibit, reduce, or prevent the synthesis of undesirable gene products.

In addition, ESTs containing the 5' ends of secretory protein genes or extended cDNAs which include sequences adjacent to the sequences of the ESTs may include sequences useful as probes for chromosome mapping and the identification of individuals. Thus, there is a need to identify and characterize the sequences upstream of the 5' coding sequences of genes encoding secretory proteins.

Summary of the Invention

The present invention relates to purified, isolated, or recombinant extended cDNAs which encode secreted proteins or fragments thereof. Preferably, the purified, isolated or recombinant cDNAs contain the entire open reading frame of their corresponding mRNAs, including a start codon and a stop codon. For example, the extended cDNAs may include nucleic acids encoding the signal peptide as well as the mature protein. Alternatively, the extended cDNAs may contain a fragment of the open reading frame. In some embodiments, the fragment may encode only the sequence of the mature protein. Alternatively, the

fragment may encode only a portion of the mature protein. A further aspect of the present invention is a nucleic acid which encodes the signal peptide of a secreted protein.

The present extended cDNAs were obtained using ESTs which include sequences derived from the authentic 5' ends of their corresponding mRNAs. As used herein the terms "EST" or "5' EST" refer to the short cDNAs which were used to obtain the extended cDNAs of the present invention. As used herein, the term "extended cDNA" refers to the cDNAs which include sequences adjacent to the 5' EST used to obtain them. The extended cDNAs may contain all or a portion of the sequence of the EST which was used to obtain them. The term "corresponding mRNA" refers to the mRNA which was the template for the cDNA synthesis which produced the 5' EST. As used herein, the term "purified" does not require absolute purity; rather, it is intended as a relative definition. Individual extended cDNA clones isolated from a cDNA library have been conventionally purified to electrophoretic homogeneity. The sequences obtained from these clones could not be obtained directly either from the library or from total human DNA. The extended cDNA clones are not naturally occurring as such, but rather are obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The conversion of mRNA into a cDNA library involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection. Thus, creating a cDNA library from messenger RNA and subsequently isolating individual clones from that library results in an approximately 10^4 - 10^6 fold purification of the native message. Purification of starting material or natural material to at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

As used herein, the term "isolated" requires that the material be removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide present in a living animal is not isolated, but the same polynucleotide, separated from some or all of the coexisting materials in the natural system, is isolated.

As used herein, the term "recombinant" means that the extended cDNA is adjacent to "backbone" nucleic acid to which it is not adjacent in its natural environment. Additionally, to be "enriched" the extended cDNAs will represent 5% or more of the number of nucleic acid inserts in a population of nucleic acid backbone molecules. Backbone molecules according to the present invention include nucleic acids such as expression vectors, self-replicating nucleic acids, viruses, integrating nucleic acids, and other vectors or nucleic acids used to maintain or manipulate a nucleic acid insert of interest. Preferably, the enriched extended cDNAs represent 15% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. More preferably, the enriched extended cDNAs represent 50% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. In a highly preferred embodiment, the enriched extended cDNAs represent 90% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. "Stringent", "moderate," and "low" hybridization conditions are as defined in Example 29.

Unless otherwise indicated, a "complementary" sequence is fully complementary. Thus, extended cDNAs encoding secreted polypeptides or fragments thereof which are present in cDNA libraries in which one or more extended cDNAs encoding secreted polypeptides or fragments thereof make up 5% or more of the number of nucleic acid inserts in the backbone molecules are "enriched recombinant extended cDNAs" as defined herein. Likewise, extended cDNAs encoding secreted polypeptides or fragments thereof which are in a population of plasmids in which one or more extended cDNAs of the present invention have been inserted such that they represent 5% or more of the number of inserts in the plasmid backbone are "enriched recombinant extended cDNAs" as defined herein. However, extended cDNAs encoding secreted polypeptides or fragments thereof which are in cDNA libraries in which the extended cDNAs encoding secreted polypeptides or fragments thereof constitute less than 5% of the number of nucleic acid inserts in the population of backbone molecules, such as libraries in which backbone molecules having a cDNA insert encoding a secreted polypeptide are extremely rare, are not "enriched recombinant extended cDNAs."

In particular, the present invention relates to extended cDNAs which were derived from genes encoding secreted proteins. As used herein, a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal peptides in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g. soluble proteins), or partially (e.g. receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Extended cDNAs encoding secreted proteins may include nucleic acid sequences, called signal sequences, which encode signal peptides which direct the extracellular secretion of the proteins encoded by the extended cDNAs. Generally, the signal peptides are located at the amino termini of secreted proteins.

Secreted proteins are translated by ribosomes associated with the "rough" endoplasmic reticulum. Generally, secreted proteins are co-translationally transferred to the membrane of the endoplasmic reticulum. Association of the ribosome with the endoplasmic reticulum during translation of secreted proteins is mediated by the signal peptide. The signal peptide is typically cleaved following its co-translational entry into the endoplasmic reticulum. After delivery to the endoplasmic reticulum, secreted proteins may proceed through the Golgi apparatus. In the Golgi apparatus, the proteins may undergo post-translational modification before entering secretory vesicles which transport them across the cell membrane.

The extended cDNAs of the present invention have several important applications. For example, they may be used to express the entire secreted protein which they encode. Alternatively, they may be used to express portions of the secreted protein. The portions may comprise the signal peptides encoded by the extended cDNAs or the mature proteins encoded by the extended cDNAs (i.e. the proteins generated when the signal peptide is cleaved off). The portions may also comprise polypeptides having at least 10 consecutive amino acids encoded by the extended cDNAs. Alternatively, the portions may comprise at least 15 consecutive amino acids encoded by the extended cDNAs. In some embodiments, the portions may

comprise at least 25 consecutive amino acids encoded by the extended cDNAs. In other embodiments, the portions may comprise at least 40 amino acids encoded by the extended cDNAs.

Antibodies which specifically recognize the entire secreted proteins encoded by the extended cDNAs or fragments thereof having at least 10 consecutive amino acids, at least 15 consecutive amino acids, at least 25 consecutive amino acids, or at least 40 consecutive amino acids may also be obtained as described below. Antibodies which specifically recognize the mature protein generated when the signal peptide is cleaved may also be obtained as described below. Similarly, antibodies which specifically recognize the signal peptides encoded by the extended cDNAs may also be obtained.

In some embodiments, the extended cDNAs include the signal sequence. In other embodiments, the extended cDNAs may include the full coding sequence for the mature protein (i.e. the protein generated when the signal polypeptide is cleaved off). In addition, the extended cDNAs may include regulatory regions upstream of the translation start site or downstream of the stop codon which control the amount, location, or developmental stage of gene expression. As discussed above, secreted proteins are therapeutically important. Thus, the proteins expressed from the cDNAs may be useful in treating or controlling a variety of human conditions. The extended cDNAs may also be used to obtain the corresponding genomic DNA. The term "corresponding genomic DNA" refers to the genomic DNA which encodes mRNA which includes the sequence of one of the strands of the extended cDNA in which thymidine residues in the sequence of the extended cDNA are replaced by uracil residues in the mRNA.

The extended cDNAs or genomic DNAs obtained therefrom may be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes corresponding to the extended cDNAs. In addition, the present invention is useful for constructing a high resolution map of the human chromosomes.

The present invention also relates to secretion vectors capable of directing the secretion of a protein of interest. Such vectors may be used in gene therapy strategies in which it is desired to produce a gene product in one cell which is to be delivered to another location in the body. Secretion vectors may also facilitate the purification of desired proteins.

The present invention also relates to expression vectors capable of directing the expression of an inserted gene in a desired spatial or temporal manner or at a desired level. Such vectors may include sequences upstream of the extended cDNAs such as promoters or upstream regulatory sequences.

In addition, the present invention may also be used for gene therapy to control or treat genetic diseases. Signal peptides may also be fused to heterologous proteins to direct their extracellular secretion.

One embodiment of the present invention is a purified or isolated nucleic acid comprising the sequence of one of SEQ ID NOs: 134-180 or a sequence complementary thereto. In one aspect of this embodiment, the nucleic acid is recombinant.

Another embodiment of the present invention is a purified or isolated nucleic acid comprising at least 10 consecutive bases of the sequence of one of SEQ ID NOs: 134-180 or one of the sequences

complementary thereto. In one aspect of this embodiment, the nucleic acid comprises at least 15, 25, 30, 40, 50, 75, or 100 consecutive bases of one of the sequences of SEQ ID NOs: 134-180 or one of the sequences complementary thereto. The nucleic acid may be a recombinant nucleic acid.

Another embodiment of the present invention is a purified or isolated nucleic acid of at least 15 bases capable of hybridizing under stringent conditions to the sequence of one of SEQ ID NOs: 134-180 or a sequence complementary to one of the sequences of SEQ ID NOs: 134-180. In one aspect of this embodiment, the nucleic acid is recombinant.

Another embodiment of the present invention is a purified or isolated nucleic acid comprising the full coding sequences of one of SEQ ID NOs: 134-180, wherein the full coding sequence optionally comprises the sequence encoding signal peptide as well as the sequence encoding mature protein. In one aspect of this embodiment, the nucleic acid is recombinant.

A further embodiment of the present invention is a purified or isolated nucleic acid comprising the nucleotides of one of SEQ ID NOs: 134-180 which encode a mature protein. In one aspect of this embodiment, the nucleic acid is recombinant.

Yet another embodiment of the present invention is a purified or isolated nucleic acid comprising the nucleotides of one of SEQ ID NOs: 134-180 which encode the signal peptide. In one aspect of this embodiment, the nucleic acid is recombinant.

Another embodiment of the present invention is a purified or isolated nucleic acid encoding a polypeptide having the sequence of one of the sequences of SEQ ID NOs: 181-227.

Another embodiment of the present invention is a purified or isolated nucleic acid encoding a polypeptide having the sequence of a mature protein included in one of the sequences of SEQ ID NOs: 181-227.

Another embodiment of the present invention is a purified or isolated nucleic acid encoding a polypeptide having the sequence of a signal peptide included in one of the sequences of SEQ ID NOs: 181-227.

Yet another embodiment of the present invention is a purified or isolated protein comprising the sequence of one of SEQ ID NOs: 181-227.

Another embodiment of the present invention is a purified or isolated polypeptide comprising at least 10 consecutive amino acids of one of the sequences of SEQ ID NOs: 181-227. In one aspect of this embodiment, the purified or isolated polypeptide comprises at least 15, 20, 25, 35, 50, 75, 100, 150 or 200 consecutive amino acids of one of the sequences of SEQ ID NOs: 181-227. In still another aspect, the purified or isolated polypeptide comprises at least 25 consecutive amino acids of one of the sequences of SEQ ID NOs: 181-227.

Another embodiment of the present invention is an isolated or purified polypeptide comprising a signal peptide of one of the polypeptides of SEQ ID NOs: 181-227.

Yet another embodiment of the present invention is an isolated or purified polypeptide comprising a

mature protein of one of the polypeptides of SEQ ID NOs: 181-227.

A further embodiment of the present invention is a method of making a protein comprising one of the sequences of SEQ ID NO: 181-227, comprising the steps of obtaining a cDNA comprising one of the sequences of sequence of SEQ ID NO: 134-180, inserting the cDNA in an expression vector such that the cDNA is operably linked to a promoter, and introducing the expression vector into a host cell whereby the host cell produces the protein encoded by said cDNA. In one aspect of this embodiment, the method further comprises the step of isolating the protein.

Another embodiment of the present invention is a protein obtainable by the method described in the preceding paragraph.

Another embodiment of the present invention is a method of making a protein comprising the amino acid sequence of the mature protein contained in one of the sequences of SEQ ID NO: 181-227, comprising the steps of obtaining a cDNA comprising one of the nucleotides sequence of sequence of SEQ ID NO: 134-180 which encode for the mature protein, inserting the cDNA in an expression vector such that the cDNA is operably linked to a promoter, and introducing the expression vector into a host cell whereby the host cell produces the mature protein encoded by the cDNA. In one aspect of this embodiment, the method further comprises the step of isolating the protein.

Another embodiment of the present invention is a mature protein obtainable by the method described in the preceding paragraph.

Another embodiment of the present invention is a host cell containing the purified or isolated nucleic acids comprising the sequence of one of SEQ ID NOs: 134-180 or a sequence complementary thereto described herein.

Another embodiment of the present invention is a host cell containing the purified or isolated nucleic acids comprising the full coding sequences of one of SEQ ID NOs: 134-180, wherein the full coding sequence comprises the sequence encoding signal peptide and the sequence encoding mature protein described herein.

Another embodiment of the present invention is a host cell containing the purified or isolated nucleic acids comprising the nucleotides of one of SEQ ID NOs: 134-180 which encode a mature protein which are described herein.

Another embodiment of the present invention is a host cell containing the purified or isolated nucleic acids comprising the nucleotides of one of SEQ ID NOs: 134-180 which encode the signal peptide which are described herein.

Another embodiment of the present invention is a purified or isolated antibody capable of specifically binding to a protein having the sequence of one of SEQ ID NOs: 181-227. In one aspect of this embodiment, the antibody is capable of binding to a polypeptide comprising at least 10 consecutive amino acids of the sequence of one of SEQ ID NOs: 181-227.

Another embodiment of the present invention is an array of cDNAs or fragments thereof of at least

15 nucleotides in length which includes at least one of the sequences of SEQ ID NOs: 134-180, or one of the sequences complementary to the sequences of SEQ ID NOs: 134-180, or a fragment thereof of at least 15 consecutive nucleotides. In one aspect of this embodiment, the array includes at least two of the sequences of SEQ ID NOs: 134-180, the sequences complementary to the sequences of SEQ ID NOs: 134-180, or fragments thereof of at least 15 consecutive nucleotides. In another aspect of this embodiment, the array includes at least five of the sequences of SEQ ID NOs: 134-180, the sequences complementary to the sequences of SEQ ID NOs: 134-180, or fragments thereof of at least 15 consecutive nucleotides.

A further embodiment of the invention encompasses purified polynucleotides comprising an insert from a clone deposited in ATCC accession No. 98619 or a fragment thereof comprising a contiguous span of at least 8, 10, 12, 15, 20, 25, 40, 60, 100, or 200 nucleotides of said insert. An additional embodiment of the invention encompasses purified polypeptides which comprise, consist of, or consist essentially of an amino acid sequence encoded by the insert from a clone deposited in ATCC accession No. 98619, as well as polypeptides which comprise a fragment of said amino acid sequence consisting of a signal peptide, a mature protein, or a contiguous span of at least 5, 8, 10, 12, 15, 20, 25, 40, 60, 100, or 200 amino acids encoded by said insert.

An additional embodiment of the invention encompasses purified polypeptides which comprise a contiguous span of at least 5, 8, 10, 12, 15, 20, 25, 40, 60, 100, or 200 amino acids of SEQ ID NOs: 185, 186, 191, 192, 200, 201, 213, 214, 215, or 227, wherein said contiguous span comprises at least one of the amino acid positions which was not shown to be identical to a public sequence in any of Figures 9 to 16. Also encompassed by the invention are purified polynucleotides encoding said polypeptides.

Brief Description of the Drawings

Figure 1 is a summary of a procedure for obtaining cDNAs which have been selected to include the 5' ends of the mRNAs from which they are derived.

Figure 2 is an analysis of the 43 amino terminal amino acids of all human SwissProt proteins to determine the frequency of false positives and false negatives using the techniques for signal peptide identification described herein.

Figure 3 shows the distribution of von Heijne scores for 5' ESTs in each of the categories described herein and the probability that these 5' ESTs encode a signal peptide.

Figure 4 shows the distribution of 5' ESTs in each category and the number of 5' ESTs in each category having a given minimum von Heijne's score.

Figure 5 shows the tissues from which the mRNAs corresponding to the 5' ESTs in each of the categories described herein were obtained.

Figure 6 is a map of pED6dpc2.

Figure 7 provides a schematic description of the promoters isolated and the way they are assembled with the corresponding 5' tags.

Figure 8 describes the transcription factor binding sites present in each of these promoters.

Figure 9 depicts an amino acid alignment between SEQ ID NO: 214 and murine SH3BGRL (AF042081). Identities are shown by (:) and conservative substitutions by (.). Cell attachment motif (RGD) is in bold type and the proline rich region is underlined.

Figure 10 depicts a multiple amino acid alignment between SEQ ID NOs: 185 and 215, and murine MEK binding partner (AF082526). Positions conserved in all three proteins are indicated by (*).

Figure 11 depicts an amino acid alignment between SEQ ID NO: 186 and murine claudin-2 (AF072128). Identities are shown by (:) and conservative substitutions by (.).

Figure 12 depicts an amino acid alignment between SEQ ID NO: 213 and GMF- γ (AB001993). In the alignment present the translation starts at position 2 of SEQ ID NO: 166. The actual start methionine of SEQ ID NO: 213 appears to be at position 13. Identities are shown by (:) and conservative substitutions by (.).

Figure 13 depicts an amino acid alignment between SEQ ID NO: 191 and Derwent Protein Sequence Database Accession NO: W36955. Identities are shown by (:) and conservative substitutions by (.).

Figure 14 depicts an amino acid alignment between SEQ ID NO: 200 and human Ring zinc finger protein (AF037204). Amino acids defining an EGF-like domain are highlighted. The region defining an almost perfect Ring Finger domain is boxed. Identities are shown by (:) and conservative substitutions by (.).

Figure 15 depicts an amino acid alignment between SEQ ID NO: 192 and Y15286. Identities are shown by (:) and conservative substitutions by (.).

Figure 16 depicts a multiple amino acid alignment between SEQ ID NOs: 201 and 227, and human stomatin (x85116). Positions conserved in all three proteins are indicated by (*). The amino acid sequences in SEQ ID NOs: 201 and 227 differ in their N-terminal sequences: segment 1-76 (SEQ ID NO: 201) and segment 1-26 (SEQ ID NO: 227). The remainder of these 2 proteins are 99.5% identical. The band 7 protein family signature is boxed. The microbody C-terminal targeting signal appears in bold type.

Detailed Description of the Preferred Embodiment

I. Obtaining 5' ESTs

The present extended cDNAs were obtained using 5' ESTs which were isolated as described below.

A. Chemical Methods for Obtaining mRNAs having Intact 5' Ends

In order to obtain the 5' ESTs used to obtain the extended cDNAs of the present invention, mRNAs having intact 5' ends must be obtained. Currently, there are two approaches for obtaining such mRNAs. One of these approaches is a chemical modification method involving derivatization of the 5' ends of the mRNAs and selection of the derivatized mRNAs. The 5' ends of eukaryotic mRNAs possess a structure referred to as a "cap" which comprises a guanosine methylated at the 7 position. The cap is joined to the

first transcribed base of the mRNA by a 5', 5'-triphosphate bond. In some instances, the 5' guanosine is methylated in both the 2 and 7 positions. Rarely, the 5' guanosine is trimethylated at the 2, 7 and 7 positions. In the chemical method for obtaining mRNAs having intact 5' ends, the 5' cap is specifically derivatized and coupled to a reactive group on an immobilizing substrate. This specific derivatization is based on the fact that only the ribose linked to the methylated guanosine at the 5' end of the mRNA and the ribose linked to the base at the 3' terminus of the mRNA, possess 2', 3'-cis diols. Optionally, where the 3' terminal ribose has a 2', 3'-cis diol, the 2', 3'-cis diol at the 3' end may be chemically modified, substituted, converted, or eliminated, leaving only the ribose linked to the methylated guanosine at the 5' end of the mRNA with a 2', 3'-cis diol. A variety of techniques are available for eliminating the 2', 3'-cis diol on the 3' terminal ribose. For example, controlled alkaline hydrolysis may be used to generate mRNA fragments in which the 3' terminal ribose is a 3'-phosphate, 2'-phosphate or (2', 3')-cyclophosphate. Thereafter, the fragment which includes the original 3' ribose may be eliminated from the mixture through chromatography on an oligo-dT column. Alternatively, a base which lacks the 2', 3'-cis diol may be added to the 3' end of the mRNA using an RNA ligase such as T4 RNA ligase. Example 1 below describes a method for ligation of pCp to the 3' end of messenger RNA.

EXAMPLE 1

Ligation of the Nucleoside Diphosphate pCp to the 3' End of Messenger RNA.

1 µg of RNA was incubated in a final reaction medium of 10 µl in the presence of 5 U of T₄ phage RNA ligase in the buffer provided by the manufacturer (Gibco - BRL), 40 U of the RNase inhibitor RNasin (Promega) and, 2 µl of ³²pCp (Amersham #PB 10208). The incubation was performed at 37°C for 2 hours or overnight at 7-8°C.

Following modification or elimination of the 2', 3'-cis diol at the 3' ribose, the 2', 3'-cis diol present at the 5' end of the mRNA may be oxidized using reagents such as NaBH₄, NaBH₃CN, or sodium periodate, thereby converting the 2', 3'-cis diol to a dialdehyde. Example 2 describes the oxidation of the 2', 3'-cis diol at the 5' end of the mRNA with sodium periodate.

EXAMPLE 2

Oxidation of 2', 3'-cis diol at the 5' End of the mRNA

0.1 OD unit of either a capped oligoribonucleotide of 47 nucleotides (including the cap) or an uncapped oligoribonucleotide of 46 nucleotides were treated as follows. The oligoribonucleotides were produced by in vitro transcription using the transcription kit "AmpliScribe T7" (Epicentre Technologies). As indicated below, the DNA template for the RNA transcript contained a single cytosine. To synthesize the uncapped RNA, all four NTPs were included in the in vitro transcription reaction. To obtain the capped RNA, GTP was replaced by an analogue of the cap, m⁷G(5')ppp(5')G. This compound, recognized by polymerase, was incorporated into the 5' end of the nascent transcript during the step of initiation of

transcription but was not capable of incorporation during the extension step. Consequently, the resulting RNA contained a cap at its 5' end. The sequences of the oligoribonucleotides produced by the in vitro transcription reaction were:

+Cap:

5 5'm7GpppGCAUCCUACUCCCAUCCAAUUCCACCCUAACUCCUCCCAUCUCCAC-3' (SEQ ID NO:1)

-Cap:

5'-pppGCAUCCUACUCCCAUCCAAUUCCACCCUAACUCCUCCCAUCUCCAC-3' (SEQ ID NO:2)

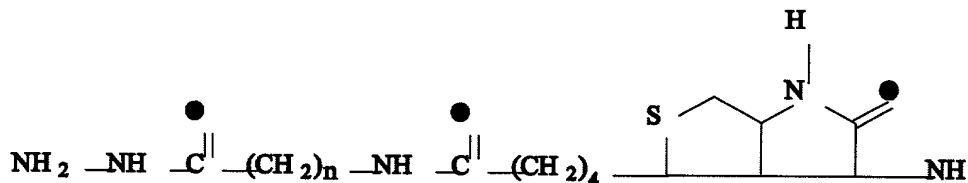
10 The oligoribonucleotides were dissolved in 9 μ l of acetate buffer (0.1 M sodium acetate, pH 5.2) and 3 μ l of freshly prepared 0.1 M sodium periodate solution. The mixture was incubated for 1 hour in the dark at 4°C or room temperature. Thereafter, the reaction was stopped by adding 4 μ l of 10% ethylene glycol. The product was ethanol precipitated, resuspended in 10 μ l or more of water or appropriate buffer and dialyzed against water.

15 The resulting aldehyde groups may then be coupled to molecules having a reactive amine group, such as hydrazine, carbazide, thiocarbazide or semicarbazide groups, in order to facilitate enrichment of the 5' ends of the mRNAs. Molecules having reactive amine groups which are suitable for use in selecting mRNAs having intact 5' ends include avidin, proteins, antibodies, vitamins, ligands capable of specifically binding to receptor molecules, or oligonucleotides. Example 3 below describes the coupling of the resulting dialdehyde to biotin.

EXAMPLE 3

Coupling of the Dialdehyde with Biotin

20 The oxidation product obtained in Example 2 was dissolved in 50 μ l of sodium acetate at a pH of between 5 and 5.2 and 50 μ l of freshly prepared 0.02 M solution of biotin hydrazide in a methoxyethanol/water mixture (1:1) of formula:



In the compound used in these experiments, n=5, and the solid black dots represent oxygen. However, it will be appreciated that other commercially available hydrazides may also be used, such as molecules of the formula above in which n varies from 0 to 5.

30 The mixture was then incubated for 2 hours at 37°C. Following the incubation, the mixture was precipitated with ethanol and dialyzed against distilled water.

Example 4 demonstrates the specificity of the biotinylation reaction.

EXAMPLE 4

Specificity of Biotinylation

The specificity of the biotinylation for capped mRNAs was evaluated by gel electrophoresis of the following samples:

Sample 1. The 46 nucleotide uncapped in vitro transcript prepared as in Example 2 and labeled with 32 PpCp as described in Example 1.

Sample 2. The 46 nucleotide uncapped in vitro transcript prepared as in Example 2, labeled with 32 PpCp as described in Example 1, treated with the oxidation reaction of Example 2, and subjected to the biotinylation conditions of Example 3.

Sample 3. The 47 nucleotide capped in vitro transcript prepared as in Example 2 and labeled with 32 PpCp as described in Example 1.

Sample 4. The 47 nucleotide capped in vitro transcript prepared as in Example 2, labeled with 32 PpCp as described in Example 1, treated with the oxidation reaction of Example 2, and subjected to the biotinylation conditions of Example 3.

Samples 1 and 2 had identical migration rates, demonstrating that the uncapped RNAs were not oxidized and biotinylated. Sample 3 migrated more slowly than Samples 1 and 2, while Sample 4 exhibited the slowest migration. The difference in migration of the RNAs in Samples 3 and 4 demonstrates that the capped RNAs were specifically biotinylated.

In some cases, mRNAs having intact 5' ends may be enriched by binding the molecule containing a reactive amine group to a suitable solid phase substrate such as the inside of the vessel containing the mRNAs, magnetic beads, chromatography matrices, or nylon or nitrocellulose membranes. For example, where the molecule having a reactive amine group is biotin, the solid phase substrate may be coupled to avidin or streptavidin. Alternatively, where the molecule having the reactive amine group is an antibody or receptor ligand, the solid phase substrate may be coupled to the cognate antigen or receptor. Finally, where the molecule having a reactive amine group comprises an oligonucleotide, the solid phase substrate may comprise a complementary oligonucleotide.

The mRNAs having intact 5' ends may be released from the solid phase following the enrichment procedure. For example, where the dialdehyde is coupled to biotin hydrazide and the solid phase comprises streptavidin, the mRNAs may be released from the solid phase by simply heating to 95 degrees Celsius in 2% SDS. In some methods, the molecule having a reactive amine group may also be cleaved from the mRNAs having intact 5' ends following enrichment. Example 5 describes the capture of biotinylated mRNAs with streptavidin coated beads and the release of the biotinylated mRNAs from the beads following enrichment.

EXAMPLE 5Capture and Release of Biotinylated mRNAs Using Streptavidin Coated Beads

The streptavidin-coated magnetic beads were prepared according to the manufacturer's instructions (CPG Inc., USA). The biotinylated mRNAs were added to a hybridization buffer (1.5 M NaCl, pH 5 - 6).

After incubating for 30 minutes, the unbound and nonbiotinylated material was removed. The beads were washed several times in water with 1% SDS. The beads obtained were incubated for 15 minutes at 95°C in water containing 2% SDS.

Example 6 demonstrates the efficiency with which biotinylated mRNAs were recovered from the streptavidin coated beads.

EXAMPLE 6Efficiency of Recovery of Biotinylated mRNAs

The efficiency of the recovery procedure was evaluated as follows. RNAs were labeled with ^{32}pCp , oxidized, biotinylated and bound to streptavidin coated beads as described above. Subsequently, the bound RNAs were incubated for 5, 15 or 30 minutes at 95°C in the presence of 2% SDS.

The products of the reaction were analyzed by electrophoresis on 12% polyacrylamide gels under denaturing conditions (7 M urea). The gels were subjected to autoradiography. During this manipulation, the hydrazone bonds were not reduced.

Increasing amounts of nucleic acids were recovered as incubation times in 2% SDS increased, demonstrating that biotinylated mRNAs were efficiently recovered.

In an alternative method for obtaining mRNAs having intact 5' ends, an oligonucleotide which has been derivatized to contain a reactive amine group is specifically coupled to mRNAs having an intact cap. Preferably, the 3' end of the mRNA is blocked prior to the step in which the aldehyde groups are joined to the derivatized oligonucleotide, as described above, so as to prevent the derivatized oligonucleotide from being joined to the 3' end of the mRNA. For example, pCp may be attached to the 3' end of the mRNA using T4 RNA ligase. However, as discussed above, blocking the 3' end of the mRNA is an optional step. Derivatized oligonucleotides may be prepared as described below in Example 7.

EXAMPLE 7Derivatization of the Oligonucleotide

An oligonucleotide phosphorylated at its 3' end was converted to a 3' hydrazide in 3' by treatment with an aqueous solution of hydrazine or of dihydrazide of the formula $\text{H}_2\text{N}(\text{R}1)\text{NH}_2$ at about 1 to 3 M, and at pH 4.5, in the presence of a carbodiimide type agent soluble in water such as 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide at a final concentration of 0.3 M at a temperature of 8°C overnight.

The derivatized oligonucleotide was then separated from the other agents and products using a standard technique for isolating oligonucleotides.

As discussed above, the mRNAs to be enriched may be treated to eliminate the 3' OH groups which may be present thereon. This may be accomplished by enzymatic ligation of sequences lacking a 3' OH, such as pCp, as described above in Example 1. Alternatively, the 3' OH groups may be eliminated by alkaline hydrolysis as described in Example 8 below.

5

EXAMPLE 8

Alkaline Hydrolysis of mRNA

The mRNAs may be treated with alkaline hydrolysis as follows. In a total volume of 100 μ l of 0.1N sodium hydroxide, 1.5 μ g mRNA is incubated for 40 to 60 minutes at 4°C. The solution is neutralized with acetic acid and precipitated with ethanol.

10

Following the optional elimination of the 3' OH groups, the diol groups at the 5' ends of the mRNAs are oxidized as described below in Example 9.

EXAMPLE 9

Oxidation of Diols

Up to 1 OD unit of RNA was dissolved in 9 μ l of buffer (0.1 M sodium acetate, pH 6-7 or water) and 3 μ l of freshly prepared 0.1 M sodium periodate solution. The reaction was incubated for 1 h in the dark at 4°C or room temperature. Following the incubation, the reaction was stopped by adding 4 μ l of 10% ethylene glycol. Thereafter the mixture was incubated at room temperature for 15 minutes. After ethanol precipitation, the product was resuspended in 10 μ l or more of water or appropriate buffer and dialyzed against water.

15

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Following oxidation of the diol groups at the 5' ends of the mRNAs, the derivatized oligonucleotide was joined to the resulting aldehydes as described in Example 10.

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EXAMPLE 10

Reaction of Aldehydes with Derivatized Oligonucleotides

The oxidized mRNA was dissolved in an acidic medium such as 50 μ l of sodium acetate pH 4-6. 50 μ l of a solution of the derivatized oligonucleotide was added such that an mRNA:derivatized oligonucleotide ratio of 1:20 was obtained and mixture was reduced with a borohydride. The mixture was allowed to incubate for 2 h at 37°C or overnight (14 h) at 10°C. The mixture was ethanol precipitated, resuspended in 10 μ l or more of water or appropriate buffer and dialyzed against distilled water. If desired, the resulting product may be analyzed using acrylamide gel electrophoresis, HPLC analysis, or other conventional techniques.

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Following the attachment of the derivatized oligonucleotide to the mRNAs, a reverse transcription reaction may be performed as described in Example 11 below.

35

EXAMPLE 11Reverse Transcription of mRNAs

An oligodeoxyribonucleotide was derivatized as follows. 3 OD units of an oligodeoxyribonucleotide of sequence ATCAAGAATTTCGACGAGACCATTA (SEQ ID NO:3) having 5'-OH and 3'-P ends were dissolved in 70 μ l of a 1.5 M hydroxybenzotriazole solution, pH 5.3, prepared in dimethylformamide/water (75:25) containing 2 μ g of 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide. The mixture was incubated for 2 h 30 min at 22°C. The mixture was then precipitated twice in LiClO₄/acetone. The pellet was resuspended in 200 μ l of 0.25 M hydrazine and incubated at 8°C from 3 to 14 h. Following the hydrazine reaction, the mixture was precipitated twice in LiClO₄/acetone.

The messenger RNAs to be reverse transcribed were extracted from blocks of placenta having sides of 2 cm which had been stored at -80°C. The mRNA was extracted using conventional acidic phenol techniques. Oligo-dT chromatography was used to purify the mRNAs. The integrity of the mRNAs was checked by Northern-blotting.

The diol groups on 7 μ g of the placental mRNAs were oxidized as described above in Example 9. The derivatized oligonucleotide was joined to the mRNAs as described in Example 10 above except that the precipitation step was replaced by an exclusion chromatography step to remove derivatized oligodeoxyribonucleotides which were not joined to mRNAs. Exclusion chromatography was performed as follows:

10 ml of AcA34 (BioSeptra#230151) gel were equilibrated in 50 ml of a solution of 10 mM Tris pH 8.0, 300 mM NaCl, 1 mM EDTA, and 0.05% SDS. The mixture was allowed to sediment. The supernatant was eliminated and the gel was resuspended in 50 ml of buffer. This procedure was repeated 2 or 3 times.

A glass bead (diameter 3 mm) was introduced into a 2 ml disposable pipette (length 25 cm). The pipette was filled with the gel suspension until the height of the gel stabilized at 1 cm from the top of the pipette. The column was then equilibrated with 20 ml of equilibration buffer (10 mM Tris HCl pH 7.4, 20 mM NaCl).

10 μ l of the mRNA which had been reacted with the derivatized oligonucleotide were mixed in 39 μ l of 10 mM urea and 2 μ l of blue-glycerol buffer, which had been prepared by dissolving 5 mg of bromophenol blue in 60% glycerol (v/v), and passing the mixture through a filter with a filter of diameter 0.45 μ m.

The column was loaded. As soon as the sample had penetrated, equilibration buffer was added. 100 μ l fractions were collected. Derivatized oligonucleotide which had not been attached to mRNA appeared in fraction 16 and later fractions. Fractions 3 to 15 were combined and precipitated with ethanol.

The mRNAs which had been reacted with the derivatized oligonucleotide were spotted on a nylon membrane and hybridized to a radioactive probe using conventional techniques. The radioactive probe used in these hybridizations was an oligodeoxyribonucleotide of sequence TAATGGTCTCGTGCGAATTCTTGAT (SEQ ID NO:4) which was anticomplementary to the derivatized

oligonucleotide and was labeled at its 5' end with ^{32}P . 1/10th of the mRNAs which had been reacted with the derivatized oligonucleotide was spotted in two spots on the membrane and the membrane was visualized by autoradiography after hybridization of the probe. A signal was observed, indicating that the derivatized oligonucleotide had been joined to the mRNA.

The remaining 9/10 of the mRNAs which had been reacted with the derivatized oligonucleotide was reverse transcribed as follows. A reverse transcription reaction was carried out with reverse transcriptase following the manufacturer's instructions. To prime the reaction, 50 pmol of nonamers with random sequence were used.

A portion of the resulting cDNA was spotted on a positively charged nylon membrane using conventional methods. The cDNAs were spotted on the membrane after the cDNA:RNA heteroduplexes had been subjected to an alkaline hydrolysis in order to eliminate the RNAs. An oligonucleotide having a sequence identical to that of the derivatized oligonucleotide was labeled at its 5' end with ^{32}P and hybridized to the cDNA blots using conventional techniques. Single-stranded cDNAs resulting from the reverse transcription reaction were spotted on the membrane. As controls, the blot contained 1 pmol, 100 fmol, 50 fmol, 10 fmol and 1 fmol respectively of a control oligodeoxyribonucleotide of sequence identical to that of the derivatized oligonucleotide. The signal observed in the spots containing the cDNA indicated that approximately 15 fmol of the derivatized oligonucleotide had been reverse transcribed.

These results demonstrate that the reverse transcription can be performed through the cap and, in particular, that reverse transcriptase crosses the 5'-P-P-P-5' bond of the cap of eukaryotic messenger RNAs.

The single stranded cDNAs obtained after the above first strand synthesis were used as template for PCR reactions. Two types of reactions were carried out. First, specific amplification of the mRNAs for the alpha globin, dehydrogenase, pp15 and elongation factor E4 were carried out using the following pairs of oligodeoxyribonucleotide primers.

alpha-globin

GLO-S: CCG ACA AGA CCA ACG TCA AGG CCG C (SEQ ID NO:5)

GLO-As: TCA CCA GCA GGC AGT GGC TTA GGA G 3' (SEQ ID NO:6)

dehydrogenase

3 DH-S: AGT GAT TCC TGC TAC TTT GGA TGG C (SEQ ID NO:7)

3 DH-As: GCT TGG TCT TGT TCT GGA GTT TAG A (SEQ ID NO:8)

pp15

PP15-S: TCC AGA ATG GGA GAC AAG CCA ATT T (SEQ ID NO:9)

PP15-As: AGG GAG GAG GAA ACA GCG TGA GTC C (SEQ ID NO:10)

Elongation factor E4

EFA1-S: ATG GGA AAG GAA AAG ACT CAT ATC A (SEQ ID NO:11)

EF1A-As: AGC AGC AAC AAT CAG GAC AGC ACA G (SEQ ID NO:12)

Non-specific amplifications were also carried out with the antisense (_As)

oligodeoxyribonucleotides of the pairs described above and a primer chosen from the sequence of the derivatized oligodeoxyribonucleotide (ATCAAGAATTTCGCACGAGACCATTA) (SEQ ID NO:13).

A 1.5% agarose gel containing the following samples corresponding to the PCR products of reverse transcription was stained with ethidium bromide. (1/20th of the products of reverse transcription were used for each PCR reaction).

Sample 1: The products of a PCR reaction using the globin primers of SEQ ID NOs 5 and 6 in the presence of cDNA.

Sample 2: The products of a PCR reaction using the globin primers of SEQ ID NOs 5 and 6 in the absence of added cDNA.

Sample 3: The products of a PCR reaction using the dehydrogenase primers of SEQ ID NOs 7 and 8 in the presence of cDNA.

Sample 4: The products of a PCR reaction using the dehydrogenase primers of SEQ ID NOs 7 and 8 in the absence of added cDNA.

Sample 5: The products of a PCR reaction using the pp15 primers of SEQ ID NOs 9 and 10 in the presence of cDNA.

Sample 6: The products of a PCR reaction using the pp15 primers of SEQ ID NOs 9 and 10 in the absence of added cDNA.

Sample 7: The products of a PCR reaction using the EIE4 primers of SEQ ID NOs 11 and 12 in the presence of added cDNA.

Sample 8: The products of a PCR reaction using the EIE4 primers of SEQ ID NOs 11 and 12 in the absence of added cDNA.

In Samples 1, 3, 5 and 7, a band of the size expected for the PCR product was observed, indicating the presence of the corresponding sequence in the cDNA population.

PCR reactions were also carried out with the antisense oligonucleotides of the globin and dehydrogenase primers (SEQ ID NOs 6 and 8) and an oligonucleotide whose sequence corresponds to that of the derivatized oligonucleotide. The presence of PCR products of the expected size in the samples corresponding to samples 1 and 3 above indicated that the derivatized oligonucleotide had been incorporated.

The above examples summarize the chemical procedure for enriching mRNAs for those having intact 5' ends. Further detail regarding the chemical approaches for obtaining mRNAs having intact 5' ends are disclosed in International Application No. WO96/34981, published November 7, 1996.

Strategies based on the above chemical modifications to the 5' cap structure may be utilized to generate cDNAs which have been selected to include the 5' ends of the mRNAs from which they are derived. In one version of such procedures, the 5' ends of the mRNAs are modified as described above. Thereafter, a reverse transcription reaction is conducted to extend a primer complementary to the mRNA to the 5' end of the mRNA. Single stranded RNAs are eliminated to obtain a population of cDNA/mRNA

heteroduplexes in which the mRNA includes an intact 5' end. The resulting heteroduplexes may be captured on a solid phase coated with a molecule capable of interacting with the molecule used to derivatize the 5' end of the mRNA. Thereafter, the strands of the heteroduplexes are separated to recover single stranded first cDNA strands which include the 5' end of the mRNA. Second strand cDNA synthesis may then proceed using conventional techniques. For example, the procedures disclosed in WO 96/34981 or in Carninci, P. et al. High-Efficiency Full-Length cDNA Cloning by Biotinylated CAP Trapper. *Genomics* 37:327-336 (1996), may be employed to select cDNAs which include the sequence derived from the 5' end of the coding sequence of the mRNA.

Following ligation of the oligonucleotide tag to the 5' cap of the mRNA, a reverse transcription reaction is conducted to extend a primer complementary to the mRNA to the 5' end of the mRNA. Following elimination of the RNA component of the resulting heteroduplex using standard techniques, second strand cDNA synthesis is conducted with a primer complementary to the oligonucleotide tag.

Figure 1 summarizes the above procedures for obtaining cDNAs which have been selected to include the 5' ends of the mRNAs from which they are derived.

B. Enzymatic Methods for Obtaining mRNAs having Intact 5' Ends

Other techniques for selecting cDNAs extending to the 5' end of the mRNA from which they are derived are fully enzymatic. Some versions of these techniques are disclosed in Dumas Milne-Edwards J.B. (Doctoral Thesis of Paris VI University, Le clonage des ADNc complets: difficultes et perspectives nouvelles. Apports pour l'etude de la regulation de l'expression de la tryptophane hydroxylase de rat, 20 Dec. 1993), EP0 625572 and Kato et al. Construction of a Human Full-Length cDNA Bank. *Gene* 150:243-250 (1994).

Briefly, in such approaches, isolated mRNA is treated with alkaline phosphatase to remove the phosphate groups present on the 5' ends of uncapped incomplete mRNAs. Following this procedure, the cap present on full length mRNAs is enzymatically removed with a decapping enzyme such as T4 polynucleotide kinase or tobacco acid pyrophosphatase. An oligonucleotide, which may be either a DNA oligonucleotide or a DNA-RNA hybrid oligonucleotide having RNA at its 3' end, is then ligated to the phosphate present at the 5' end of the decapped mRNA using T4 RNA ligase. The oligonucleotide may include a restriction site to facilitate cloning of the cDNAs following their synthesis. Example 12 below describes one enzymatic method based on the doctoral thesis of Dumas.

EXAMPLE 12

Enzymatic Approach for Obtaining 5' ESTs

Twenty micrograms of PolyA+ RNA were dephosphorylated using Calf Intestinal Phosphatase (Biolabs). After a phenol chloroform extraction, the cap structure of mRNA was hydrolyzed using the Tobacco Acid Pyrophosphatase (purified as described by Shinshi et al., *Biochemistry* 15: 2185-2190, 1976) and a hemi 5'DNA/RNA-3' oligonucleotide having an unphosphorylated 5' end, a stretch of adenosine

ribophosphate at the 3' end, and an EcoRI site near the 5' end was ligated to the 5'P ends of mRNA using the T4 RNA ligase (Biolabs). Oligonucleotides suitable for use in this procedure are preferably 30-50 bases in length. Oligonucleotides having an unphosphorylated 5' end may be synthesized by adding a fluorochrome at the 5' end. The inclusion of a stretch of adenosine ribophosphates at the 3' end of the oligonucleotide increases ligation efficiency. It will be appreciated that the oligonucleotide may contain cloning sites other than EcoRI.

Following ligation of the oligonucleotide to the phosphate present at the 5' end of the decapped mRNA, first and second strand cDNA synthesis may be carried out using conventional methods or those specified in EP0 625,572 and Kato et al. Construction of a Human Full-Length cDNA Bank. *Gene* **150**:243-250 (1994), and Dumas Milne-Edwards, *supra*. The resulting cDNA may then be ligated into vectors such as those disclosed in Kato et al. Construction of a Human Full-Length cDNA Bank. *Gene* **150**:243-250 (1994) or other nucleic acid vectors known to those skilled in the art using techniques such as those described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* 2d Ed., Cold Spring Harbor Laboratory Press (1989).

II. Characterization of 5' ESTs

The above chemical and enzymatic approaches for enriching mRNAs having intact 5' ends were employed to obtain 5' ESTs. First, mRNAs were prepared as described in Example 13 below.

EXAMPLE 13

Preparation of mRNA

Total human RNAs or PolyA+ RNAs derived from 29 different tissues were respectively purchased from LABIMO and CLONTECH and used to generate 44 cDNA libraries as described below. The purchased RNA had been isolated from cells or tissues using acid guanidium thiocyanate-phenol-chloroform extraction (Chomczynski, P and Sacchi, N., *Analytical Biochemistry* **162**:156-159, 1987). PolyA+ RNA was isolated from total RNA (LABIMO) by two passes of oligodT chromatography, as described by Aviv and Leder (Aviv, H. and Leder, P., *Proc. Natl. Acad. Sci. USA* **69**:1408-1412, 1972) in order to eliminate ribosomal RNA.

The quality and the integrity of the poly A+ were checked. Northern blots hybridized with a globin probe were used to confirm that the mRNAs were not degraded. Contamination of the PolyA+ mRNAs by ribosomal sequences was checked using RNAs blots and a probe derived from the sequence of the 28S RNA. Preparations of mRNAs with less than 5% of ribosomal RNAs were used in library construction. To avoid constructing libraries with RNAs contaminated by exogenous sequences (prokaryotic or fungal), the presence of bacterial 16S ribosomal sequences or of two highly expressed mRNAs was examined using PCR.

Following preparation of the mRNAs, the above described chemical and/or the enzymatic procedures for enriching mRNAs having intact 5' ends discussed above were employed to obtain 5' ESTs

from various tissues. In both approaches an oligonucleotide tag was attached to the cap at the 5' ends of the mRNAs. The oligonucleotide tag had an EcoRI site therein to facilitate later cloning procedures.

Following attachment of the oligonucleotide tag to the mRNA by either the chemical or enzymatic methods, the integrity of the mRNA was examined by performing a Northern blot with 200-500ng of mRNA using a probe complementary to the oligonucleotide tag.

EXAMPLE 14

cDNA Synthesis Using mRNA Templates Having Intact 5' Ends

For the mRNAs joined to oligonucleotide tags using both the chemical and enzymatic methods, first strand cDNA synthesis was performed with reverse transcriptase using random nonamers as primers. In order to protect internal EcoRI sites in the cDNA from digestion at later steps in the procedure, methylated dCTP was used for first strand synthesis. After removal of RNA by an alkaline hydrolysis, the first strand of cDNA was precipitated using isopropanol in order to eliminate residual primers.

For both the chemical and the enzymatic methods, synthesis of the second strand of the cDNA is conducted as follows. After removal of RNA by alkaline hydrolysis, the first strand of cDNA is precipitated using isopropanol in order to eliminate residual primers. The second strand of the cDNA was synthesized with Klenow using a primer corresponding to the 5' end of the ligated oligonucleotide described in Example 12. Preferably, the primer is 20-25 bases in length. Methylated dCTP was also used for second strand synthesis in order to protect internal EcoRI sites in the cDNA from digestion during the cloning process.

Following cDNA synthesis, the cDNAs were cloned into pBlueScript as described in Example 15 below.

EXAMPLE 15

Insertion of cDNAs into BlueScript

Following second strand synthesis, the ends of the cDNA were blunted with T4 DNA polymerase (Biolabs) and the cDNA was digested with EcoRI. Since methylated dCTP was used during cDNA synthesis, the EcoRI site present in the tag was the only site which was hemi-methylated. Consequently, only the EcoRI site in the oligonucleotide tag was susceptible to EcoRI digestion. The cDNA was then size fractionated using exclusion chromatography (AcA, Biosepra). Fractions corresponding to cDNAs of more than 150 bp were pooled and ethanol precipitated. The cDNA was directionally cloned into the SmaI and EcoRI ends of the phagemid pBlueScript vector (Stratagene). The ligation mixture was electroporated into bacteria and propagated under appropriate antibiotic selection.

Clones containing the oligonucleotide tag attached were selected as described in Example 16 below.

EXAMPLE 16Selection of Clones Having the Oligonucleotide Tag Attached Thereto

The plasmid DNAs containing 5' EST libraries made as described above were purified (Qiagen). A positive selection of the tagged clones was performed as follows. Briefly, in this selection procedure, the plasmid DNA was converted to single stranded DNA using gene II endonuclease of the phage F1 in combination with an exonuclease (Chang *et al.*, *Gene* **127**:95-8, (1993)) such as exonuclease III or T7 gene 6 exonuclease. The resulting single stranded DNA was then purified using paramagnetic beads as described by Fry *et al.*, *Biotechniques*, **13**: 124-131 (1992). In this procedure, the single stranded DNA was hybridized with a biotinylated oligonucleotide having a sequence corresponding to the 3' end of the oligonucleotide described in Example 13. Preferably, the primer has a length of 20-25 bases. Clones including a sequence complementary to the biotinylated oligonucleotide were captured by incubation with streptavidin coated magnetic beads followed by magnetic selection. After capture of the positive clones, the plasmid DNA was released from the magnetic beads and converted into double stranded DNA using a DNA polymerase such as the ThermoSequenase obtained from Amersham Pharmacia Biotech. Alternatively, protocols such as the Gene Trapper kit (Gibco BRL) may be used. The double stranded DNA was then electroporated into bacteria. The percentage of positive clones having the 5' tag oligonucleotide was estimated to typically rank between 90 and 98% using dot blot analysis.

Following electroporation, the libraries were ordered in 384-microtiter plates (MTP). A copy of the MTP was stored for future needs. Then the libraries were transferred into 96 MTP and sequenced as described below.

EXAMPLE 17Sequencing of Inserts in Selected Clones

Plasmid inserts were first amplified by PCR on PE 9600 thermocyclers (Perkin-Elmer), using standard SETA-A and SETA-B primers (Genset SA), AmpliTaqGold (Perkin-Elmer), dNTPs (Boehringer), buffer and cycling conditions as recommended by the Perkin-Elmer Corporation.

PCR products were then sequenced using automatic ABI Prism 377 sequencers (Perkin Elmer, Applied Biosystems Division, Foster City, CA). Sequencing reactions were performed using PE 9600 thermocyclers (Perkin Elmer) with standard dye-primer chemistry and ThermoSequenase (Amersham Life Science). The primers used were either T7 or 21M13 (available from Genset SA) as appropriate. The primers were labeled with the JOE, FAM, ROX and TAMRA dyes. The dNTPs and ddNTPs used in the sequencing reactions were purchased from Boehringer. Sequencing buffer, reagent concentrations and cycling conditions were as recommended by Amersham.

Following the sequencing reaction, the samples were precipitated with EtOH, resuspended in formamide loading buffer, and loaded on a standard 4% acrylamide gel. Electrophoresis was performed for 2.5 hours at 3000V on an ABI 377 sequencer, and the sequence data were collected and analyzed using the

ABI Prism DNA Sequencing Analysis Software, version 2.1.2.

The sequence data from the 44 cDNA libraries made as described above were transferred to a proprietary database, where quality control and validation steps were performed. A proprietary base-caller ("Trace"), working using a Unix system automatically flagged suspect peaks, taking into account the shape of the peaks, the inter-peak resolution, and the noise level. The proprietary base-caller also performed an automatic trimming. Any stretch of 25 or fewer bases having more than 4 suspect peaks was considered unreliable and was discarded. Sequences corresponding to cloning vector or ligation oligonucleotides were automatically removed from the EST sequences. However, the resulting EST sequences may contain 1 to 5 bases belonging to the above mentioned sequences at their 5' end. If needed, these can easily be removed on a case by case basis.

Thereafter, the sequences were transferred to the proprietary NETGENE™ Database for further analysis as described below.

Following sequencing as described above, the sequences of the 5' ESTs were entered in a proprietary database called NETGENE™ for storage and manipulation. It will be appreciated by those skilled in the art that the data could be stored and manipulated on any medium which can be read and accessed by a computer. Computer readable media include magnetically readable media, optically readable media, or electronically readable media. For example, the computer readable media may be a hard disc, a floppy disc, a magnetic tape, CD-ROM, RAM, or ROM as well as other types of other media known to those skilled in the art.

In addition, the sequence data may be stored and manipulated in a variety of data processor programs in a variety of formats. For example, the sequence data may be stored as text in a word processing file, such as Microsoft WORD or WORDPERFECT or as an ASCII file in a variety of database programs familiar to those of skill in the art, such as DB2, SYBASE, or ORACLE.

The computer readable media on which the sequence information is stored may be in a personal computer, a network, a server or other computer systems known to those skilled in the art. The computer or other system preferably includes the storage media described above, and a processor for accessing and manipulating the sequence data.

Once the sequence data has been stored it may be manipulated and searched to locate those stored sequences which contain a desired nucleic acid sequence or which encode a protein having a particular functional domain. For example, the stored sequence information may be compared to other known sequences to identify homologies, motifs implicated in biological function, or structural motifs.

Programs which may be used to search or compare the stored sequences include the MacPattern (EMBL), BLAST, and BLAST2 program series (NCBI), basic local alignment search tool programs for nucleotide (BLASTN) and peptide (BLASTX) comparisons (Altschul et al, *J. Mol. Biol.* **215**: 403 (1990)) and FASTA (Pearson and Lipman, *Proc. Natl. Acad. Sci. USA*, **85**: 2444 (1988)). The BLAST programs then extend the alignments on the basis of defined match and mismatch criteria.

Motifs which may be detected using the above programs include sequences encoding leucine zippers, helix-turn-helix motifs, glycosylation sites, ubiquitination sites, alpha helices, and beta sheets, signal sequences encoding signal peptides which direct the secretion of the encoded proteins, sequences implicated in transcription regulation such as homeoboxes, acidic stretches, enzymatic active sites, substrate binding sites, and enzymatic cleavage sites.

Before searching the cDNAs in the NETGENE™ database for sequence motifs of interest, cDNAs derived from mRNAs which were not of interest were identified and eliminated from further consideration as described in Example 18 below.

EXAMPLE 18

Elimination of Undesired Sequences from Further Consideration

5' ESTs in the NETGENE™ database which were derived from undesired sequences such as transfer RNAs, ribosomal RNAs, mitochondrial RNAs, procaryotic RNAs, fungal RNAs, Alu sequences, L1 sequences, or repeat sequences were identified using the FASTA and BLASTN programs with the parameters listed in Table I.

To eliminate 5' ESTs encoding tRNAs from further consideration, the 5' EST sequences were compared to the sequences of 1190 known tRNAs obtained from EMBL release 38, of which 100 were human. The comparison was performed using FASTA on both strands of the 5' ESTs. Sequences having more than 80% homology over more than 60 nucleotides were identified as tRNA. Of the 144,341 sequences screened, 26 were identified as tRNAs and eliminated from further consideration.

To eliminate 5' ESTs encoding rRNAs from further consideration, the 5' EST sequences were compared to the sequences of 2497 known rRNAs obtained from EMBL release 38, of which 73 were human. The comparison was performed using BLASTN on both strands of the 5' ESTs with the parameter S=108. Sequences having more than 80% homology over stretches longer than 40 nucleotides were identified as rRNAs. Of the 144,341 sequences screened, 3,312 were identified as rRNAs and eliminated from further consideration.

To eliminate 5' ESTs encoding mtRNAs from further consideration, the 5' EST sequences were compared to the sequences of the two known mitochondrial genomes for which the entire genomic sequences are available and all sequences transcribed from these mitochondrial genomes including tRNAs, rRNAs, and mRNAs for a total of 38 sequences. The comparison was performed using BLASTN on both strands of the 5' ESTs with the parameter S=108. Sequences having more than 80% homology over stretches longer than 40 nucleotides were identified as mtRNAs. Of the 144,341 sequences screened, 6,110 were identified as mtRNAs and eliminated from further consideration.

Sequences which might have resulted from exogenous contaminants were eliminated from further consideration by comparing the 5' EST sequences to release 46 of the EMBL bacterial and fungal divisions using BLASTN with the parameter S=144. All sequences having more than 90% homology over at least 40

nucleotides were identified as exogenous contaminants. Of the 42 cDNA libraries examined, the average percentages of procaryotic and fungal sequences contained therein were 0.2% and 0.5% respectively. Among these sequences, only one could be identified as a sequence specific to fungi. The others were either fungal or procaryotic sequences having homologies with vertebrate sequences or including repeat sequences which had not been masked during the electronic comparison.

In addition, the 5' ESTs were compared to 6093 Alu sequences and 1115 L1 sequences to mask 5' ESTs containing such repeat sequences from further consideration. 5' ESTs including THE and MER repeats, SSTR sequences or satellite, micro-satellite, or telomeric repeats were also eliminated from further consideration. On average, 11.5% of the sequences in the libraries contained repeat sequences. Of this 11.5%, 7% contained Alu repeats, 3.3% contained L1 repeats and the remaining 1.2% were derived from the other types of repetitive sequences which were screened. These percentages are consistent with those found in cDNA libraries prepared by other groups. For example, the cDNA libraries of Adams et al. contained between 0% and 7.4% Alu repeats depending on the source of the RNA which was used to prepare the cDNA library (Adams et al., *Nature* 377:174, 1996).

The sequences of those 5' ESTs remaining after the elimination of undesirable sequences were compared with the sequences of known human mRNAs to determine the accuracy of the sequencing procedures described above.

EXAMPLE 19

Measurement of Sequencing Accuracy by Comparison to Known Sequences

To further determine the accuracy of the sequencing procedure described above, the sequences of 5' ESTs derived from known sequences were identified and compared to the known sequences. First, a FASTA analysis with overhangs shorter than 5 bp on both ends was conducted on the 5' ESTs to identify those matching an entry in the public human mRNA database. The 6655 5' ESTs which matched a known human mRNA were then realigned with their cognate mRNA and dynamic programming was used to include substitutions, insertions, and deletions in the list of "errors" which would be recognized. Errors occurring in the last 10 bases of the 5' EST sequences were ignored to avoid the inclusion of spurious cloning sites in the analysis of sequencing accuracy.

This analysis revealed that the sequences incorporated in the NETGENE™ database had an accuracy of more than 99.5%.

To determine the efficiency with which the above selection procedures select cDNAs which include the 5' ends of their corresponding mRNAs, the following analysis was performed.

EXAMPLE 20

Determination of Efficiency of 5' EST Selection

To determine the efficiency at which the above selection procedures isolated 5' ESTs which

included sequences close to the 5' end of the mRNAs from which they were derived, the sequences of the ends of the 5' ESTs which were derived from the elongation factor 1 subunit α and ferritin heavy chain genes were compared to the known cDNA sequences for these genes. Since the transcription start sites for the elongation factor 1 subunit α and ferritin heavy chain are well characterized, they may be used to determine the percentage of 5' ESTs derived from these genes which included the authentic transcription start sites.

For both genes, more than 95% of the cDNAs included sequences close to or upstream of the 5' end of the corresponding mRNAs.

To extend the analysis of the reliability of the procedures for isolating 5' ESTs from ESTs in the NETGENE™ database, a similar analysis was conducted using a database composed of human mRNA sequences extracted from GenBank database release 97 for comparison. For those 5' ESTs derived from mRNAs included in the GeneBank database, more than 85% had their 5' ends close to the 5' ends of the known sequence. As some of the mRNA sequences available in the GenBank database are deduced from genomic sequences, a 5' end matching with these sequences will be counted as an internal match. Thus, the method used here underestimates the yield of ESTs including the authentic 5' ends of their corresponding mRNAs.

The EST libraries made above included multiple 5' ESTs derived from the same mRNA. The sequences of such 5' ESTs were compared to one another and the longest 5' ESTs for each mRNA were identified. Overlapping cDNAs were assembled into continuous sequences (contigs). The resulting continuous sequences were then compared to public databases to gauge their similarity to known sequences, as described in Example 21 below.

EXAMPLE 21

Clustering of the 5' ESTs and Calculation of Novelty Indices for cDNA Libraries

For each sequenced EST library, the sequences were clustered by the 5' end. Each sequence in the library was compared to the others with BLASTN2 (direct strand, parameters S=107). ESTs with High Scoring Segment Pairs (HSPs) at least 25 bp long, having 95% identical bases and beginning closer than 10 bp from each EST 5' end were grouped. The longest sequence found in the cluster was used as representative of the cluster. A global clustering between libraries was then performed leading to the definition of super-contigs.

To assess the yield of new sequences within the EST libraries, a novelty rate (NR) was defined as: $NR = 100 \times (\text{Number of new unique sequences found in the library} / \text{Total number of sequences from the library})$. Typically, novelty rating range between 10% and 41% depending on the tissue from which the EST library was obtained. For most of the libraries, the random sequencing of 5' EST libraries was pursued until the novelty rate reached 20%.

Following characterization as described above, the collection of 5' ESTs in NETGENE™ was

screened to identify those 5' ESTs bearing potential signal sequences as described in Example 22 below.

EXAMPLE 22

Identification of Potential Signal Sequences in 5' ESTs

The 5' ESTs in the NETGENE™ database were screened to identify those having an uninterrupted open reading frame (ORF) longer than 45 nucleotides beginning with an ATG codon and extending to the end of the EST. Approximately half of the cDNA sequences in NETGENE™ contained such an ORF. The ORFs of these 5' ESTs were searched to identify potential signal motifs using slight modifications of the procedures disclosed in Von Heijne, G. A New Method for Predicting Signal Sequence Cleavage Sites.

Nucleic Acids Res. **14**:4683-4690 (1986). Those 5' EST sequences encoding a 15 amino acid long stretch with a score of at least 3.5 in the Von Heijne signal peptide identification matrix were considered to possess a signal sequence. Those 5' ESTs which matched a known human mRNA or EST sequence and had a 5' end more than 20 nucleotides downstream of the known 5' end were excluded from further analysis. The remaining cDNAs having signal sequences therein were included in a database called SIGNALTAG™.

To confirm the accuracy of the above method for identifying signal sequences, the analysis of Example 23 was performed.

EXAMPLE 23

Confirmation of Accuracy of Identification of Potential Signal Sequences in 5' ESTs

The accuracy of the above procedure for identifying signal sequences encoding signal peptides was evaluated by applying the method to the 43 amino terminal amino acids of all human SwissProt proteins. The computed Von Heijne score for each protein was compared with the known characterization of the protein as being a secreted protein or a non-secreted protein. In this manner, the number of non-secreted proteins having a score higher than 3.5 (false positives) and the number of secreted proteins having a score lower than 3.5 (false negatives) could be calculated.

Using the results of the above analysis, the probability that a peptide encoded by the 5' region of the mRNA is in fact a genuine signal peptide based on its Von Heijne's score was calculated based on either the assumption that 10% of human proteins are secreted or the assumption that 20% of human proteins are secreted. The results of this analysis are shown in Figures 2 and 3.

Using the above method of identifying secretory proteins, 5' ESTs for human glucagon, gamma interferon induced monokine precursor, secreted cyclophilin-like protein, human pleiotropin, and human biotinidase precursor all of which are polypeptides which are known to be secreted, were obtained. Thus, the above method successfully identified those 5' ESTs which encode a signal peptide.

To confirm that the signal peptide encoded by the 5' ESTs actually functions as a signal peptide, the signal sequences from the 5' ESTs may be cloned into a vector designed for the identification of signal peptides. Some signal peptide identification vectors are designed to confer the ability to grow in selective

medium on host cells which have a signal sequence operably inserted into the vector. For example, to confirm that a 5' EST encodes a genuine signal peptide, the signal sequence of the 5' EST may be inserted upstream and in frame with a non-secreted form of the yeast invertase gene in signal peptide selection vectors such as those described in U.S. Patent No. 5,536,637. Growth of host cells containing signal sequence selection vectors having the signal sequence from the 5' EST inserted therein confirms that the 5' EST encodes a genuine signal peptide.

Alternatively, the presence of a signal peptide may be confirmed by cloning the extended cDNAs obtained using the ESTs into expression vectors such as pXT1 (as described below), or by constructing promoter-signal sequence-reporter gene vectors which encode fusion proteins between the signal peptide and an assayable reporter protein. After introduction of these vectors into a suitable host cell, such as COS cells or NIH 3T3 cells, the growth medium may be harvested and analyzed for the presence of the secreted protein. The medium from these cells is compared to the medium from cells containing vectors lacking the signal sequence or extended cDNA insert to identify vectors which encode a functional signal peptide or an authentic secreted protein.

Those 5' ESTs which encoded a signal peptide, as determined by the method of Example 22 above, were further grouped into four categories based on their homology to known sequences. The categorization of the 5' ESTs is described in Example 24 below.

EXAMPLE 24

Categorization of 5' ESTs Encoding a Signal Peptide

Those 5' ESTs having a sequence not matching any known vertebrate sequence nor any publicly available EST sequence were designated "new." Of the sequences in the SIGNALTAG™ database, 947 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those 5' ESTs having a sequence not matching any vertebrate sequence but matching a publicly known EST were designated "EST-ext", provided that the known EST sequence was extended by at least 40 nucleotides in the 5' direction. Of the sequences in the SIGNALTAG™ database, 150 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those ESTs not matching any vertebrate sequence but matching a publicly known EST without extending the known EST by at least 40 nucleotides in the 5' direction were designated "EST." Of the sequences in the SIGNALTAG™ database, 599 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those 5' ESTs matching a human mRNA sequence but extending the known sequence by at least 40 nucleotides in the 5' direction were designated "VERT-ext." Of the sequences in the SIGNALTAG™ database, 23 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category. Included in this category was a 5' EST which extended the known sequence of the human translocase mRNA by more than 200 bases in the 5' direction. A 5' EST which extended the sequence of a human tumor suppressor

gene in the 5' direction was also identified.

Figure 4 shows the distribution of 5' ESTs in each category and the number of 5' ESTs in each category having a given minimum von Heijne's score.

Each of the 5' ESTs was categorized based on the tissue from which its corresponding mRNA was obtained, as described below in Example 25.

EXAMPLE 25

Categorization of Expression Patterns

Figure 5 shows the tissues from which the mRNAs corresponding to the 5' ESTs in each of the above described categories were obtained.

In addition to categorizing the 5' ESTs by the tissue from which the cDNA library in which they were first identified was obtained, the spatial and temporal expression patterns of the mRNAs corresponding to the 5' ESTs, as well as their expression levels, may be determined as described in Example 26 below. Characterization of the spatial and temporal expression patterns and expression levels of these mRNAs is useful for constructing expression vectors capable of producing a desired level of gene product in a desired spatial or temporal manner, as will be discussed in more detail below.

In addition, 5' ESTs whose corresponding mRNAs are associated with disease states may also be identified. For example, a particular disease may result from lack of expression, over expression, or under expression of an mRNA corresponding to a 5' EST. By comparing mRNA expression patterns and quantities in samples taken from healthy individuals with those from individuals suffering from a particular disease, 5' ESTs responsible for the disease may be identified.

It will be appreciated that the results of the above characterization procedures for 5' ESTs also apply to extended cDNAs (obtainable as described below) which contain sequences adjacent to the 5' ESTs.

It will also be appreciated that if it is desired to defer characterization until extended cDNAs have been obtained rather than characterizing the ESTs themselves, the above characterization procedures can be applied to characterize the extended cDNAs after their isolation.

EXAMPLE 26

Evaluation of Expression Levels and Patterns of mRNAs

Corresponding to 5' ESTs or Extended cDNAs

Expression levels and patterns of mRNAs corresponding to 5' ESTs or extended cDNAs (obtainable as described below) may be analyzed by solution hybridization with long probes as described in International Patent Application No. WO 97/05277. Briefly, a 5' EST, extended cDNA, or fragment thereof corresponding to the gene encoding the mRNA to be characterized is inserted at a cloning site immediately downstream of a bacteriophage (T3, T7 or SP6) RNA polymerase promoter to produce antisense RNA. Preferably, the 5' EST or extended cDNA has 100 or more nucleotides. The plasmid is linearized and

transcribed in the presence of ribonucleotides comprising modified ribonucleotides (i.e. biotin-UTP and DIG-UTP). An excess of this doubly labeled RNA is hybridized in solution with mRNA isolated from cells or tissues of interest. The hybridizations are performed under standard stringent conditions (40-50°C for 16 hours in an 80% formamide, 0.4 M NaCl buffer, pH 7-8). The unhybridized probe is removed by digestion with ribonucleases specific for single-stranded RNA (i.e. RNases CL3, T1, Phy M, U2 or A). The presence of the biotin-UTP modification enables capture of the hybrid on a microtitration plate coated with streptavidin. The presence of the DIG modification enables the hybrid to be detected and quantified by ELISA using an anti-DIG antibody coupled to alkaline phosphatase.

The 5' ESTs, extended cDNAs, or fragments thereof may also be tagged with nucleotide sequences for the serial analysis of gene expression (SAGE) as disclosed in UK Patent Application No. 2,305,241 A. In this method, cDNAs are prepared from a cell, tissue, organism or other source of nucleic acid for which it is desired to determine gene expression patterns. The resulting cDNAs are separated into two pools. The cDNAs in each pool are cleaved with a first restriction endonuclease, called an "anchoring enzyme," having a recognition site which is likely to be present at least once in most cDNAs. The fragments which contain the 5' or 3' most region of the cleaved cDNA are isolated by binding to a capture medium such as streptavidin coated beads. A first oligonucleotide linker having a first sequence for hybridization of an amplification primer and an internal restriction site for a "tagging endonuclease" is ligated to the digested cDNAs in the first pool. Digestion with the second endonuclease produces short "tag" fragments from the cDNAs.

A second oligonucleotide having a second sequence for hybridization of an amplification primer and an internal restriction site is ligated to the digested cDNAs in the second pool. The cDNA fragments in the second pool are also digested with the "tagging endonuclease" to generate short "tag" fragments derived from the cDNAs in the second pool. The "tags" resulting from digestion of the first and second pools with the anchoring enzyme and the tagging endonuclease are ligated to one another to produce "ditags." In some embodiments, the ditags are concatamerized to produce ligation products containing from 2 to 200 ditags. The tag sequences are then determined and compared to the sequences of the 5' ESTs or extended cDNAs to determine which 5' ESTs or extended cDNAs are expressed in the cell, tissue, organism, or other source of nucleic acids from which the tags were derived. In this way, the expression pattern of the 5' ESTs or extended cDNAs in the cell, tissue, organism, or other source of nucleic acids is obtained.

Quantitative analysis of gene expression may also be performed using arrays. As used herein, the term array means a one dimensional, two dimensional, or multidimensional arrangement of full length cDNAs (i.e. extended cDNAs which include the coding sequence for the signal peptide, the coding sequence for the mature protein, and a stop codon), extended cDNAs, 5' ESTs or fragments of the full length cDNAs, extended cDNAs, or 5' ESTs of sufficient length to permit specific detection of gene expression. Preferably, the fragments are at least 15 nucleotides in length. More preferably, the fragments are at least 100 nucleotides in length. More preferably, the fragments are more than 100 nucleotides in

length. In some embodiments the fragments may be more than 500 nucleotides in length.

For example, quantitative analysis of gene expression may be performed with full length cDNAs, extended cDNAs, 5' ESTs, or fragments thereof in a complementary DNA microarray as described by Schena et al. *Science* **270**:467-470, 1995; *Proc. Natl. Acad. Sci. U.S.A.* **93**:10614-10619 (1996). Full length cDNAs, extended cDNAs, 5' ESTs or fragments thereof are amplified by PCR and arrayed from 96-well microtiter plates onto silylated microscope slides using high-speed robotics. Printed arrays are incubated in a humid chamber to allow rehydration of the array elements and rinsed, once in 0.2% SDS for 1 min, twice in water for 1 min and once for 5 min in sodium borohydride solution. The arrays are submerged in water for 2 min at 95°C, transferred into 0.2% SDS for 1 min, rinsed twice with water, air dried and stored in the dark at 25°C.

Cell or tissue mRNA is isolated or commercially obtained and probes are prepared by a single round of reverse transcription. Probes are hybridized to 1 cm² microarrays under a 14 x 14 mm glass coverslip for 6-12 hours at 60°C. Arrays are washed for 5 min at 25°C in low stringency wash buffer (1 x SSC/0.2% SDS), then for 10 min at room temperature in high stringency wash buffer (0.1 x SSC/0.2% SDS). Arrays are scanned in 0.1 x SSC using a fluorescence laser scanning device fitted with a custom filter set. Accurate differential expression measurements are obtained by taking the average of the ratios of two independent hybridizations.

Quantitative analysis of the expression of genes may also be performed with full length cDNAs, extended cDNAs, 5' ESTs, or fragments thereof in complementary DNA arrays as described by Pietu et al. *Genome Research* **6**:492-503 (1996). The full length cDNAs, extended cDNAs, 5' ESTs or fragments thereof are PCR amplified and spotted on membranes. Then, mRNAs originating from various tissues or cells are labeled with radioactive nucleotides. After hybridization and washing in controlled conditions, the hybridized mRNAs are detected by phospho-imaging or autoradiography. Duplicate experiments are performed and a quantitative analysis of differentially expressed mRNAs is then performed.

Alternatively, expression analysis of the 5' ESTs or extended cDNAs can be done through high density nucleotide arrays as described by Lockhart et al. *Nature Biotechnology* **14**: 1675-1680, 1996. and Sosnowsky et al. *Proc. Natl. Acad. Sci.* **94**:1119-1123, 1997. Oligonucleotides of 15-50 nucleotides corresponding to sequences of the 5' ESTs or extended cDNAs are synthesized directly on the chip (Lockhart et al., *supra*) or synthesized and then addressed to the chip (Sosnowski et al., *supra*). Preferably, the oligonucleotides are about 20 nucleotides in length.

cDNA probes labeled with an appropriate compound, such as biotin, digoxigenin or fluorescent dye, are synthesized from the appropriate mRNA population and then randomly fragmented to an average size of 50 to 100 nucleotides. The said probes are then hybridized to the chip. After washing as described in Lockhart et al., *supra* and application of different electric fields (Sosnowsky et al., *Proc. Natl. Acad. Sci.* **94**:1119-1123), the dyes or labeling compounds are detected and quantified. Duplicate hybridizations are performed. Comparative analysis of the intensity of the signal originating from cDNA probes on the same

target oligonucleotide in different cDNA samples indicates a differential expression of the mRNA corresponding to the 5' EST or extended cDNA from which the oligonucleotide sequence has been designed.

III. Use of 5' ESTs to Clone Extended cDNAs and to Clone the Corresponding Genomic DNAs

Once 5' ESTs which include the 5' end of the corresponding mRNAs have been selected using the procedures described above, they can be utilized to isolate extended cDNAs which contain sequences adjacent to the 5' ESTs. The extended cDNAs may include the entire coding sequence of the protein encoded by the corresponding mRNA, including the authentic translation start site, the signal sequence, and the sequence encoding the mature protein remaining after cleavage of the signal peptide. Such extended cDNAs are referred to herein as "full length cDNAs." Alternatively, the extended cDNAs may include only the sequence encoding the mature protein remaining after cleavage of the signal peptide, or only the sequence encoding the signal peptide.

Example 27 below describes a general method for obtaining extended cDNAs. Example 28 below describes the cloning and sequencing of several extended cDNAs, including extended cDNAs which include the entire coding sequence and authentic 5' end of the corresponding mRNA for several secreted proteins.

The methods of Examples 27, 28, and 29 can also be used to obtain extended cDNAs which encode less than the entire coding sequence of the secreted proteins encoded by the genes corresponding to the 5' ESTs. In some embodiments, the extended cDNAs isolated using these methods encode at least 10 amino acids of one of the proteins encoded by the sequences of SEQ ID NOs: 134-180. In further embodiments, the extended cDNAs encode at least 20 amino acids of the proteins encoded by the sequences of SEQ ID NOs: 134-180. In further embodiments, the extended cDNAs encode at least 30 amino acids of the sequences of SEQ ID NOs: 134-180. In a preferred embodiment, the extended cDNAs encode a full length protein sequence, which includes the protein coding sequences of SEQ ID NOs: 134-180.

EXAMPLE 27

General Method for Using 5' ESTs to Clone and Sequence Extended cDNAs which Include the Entire Coding Region and the Authentic 5' End of the Corresponding mRNA

The following general method has been used to quickly and efficiently isolate extended cDNAs including sequence adjacent to the sequences of the 5' ESTs used to obtain them. This method may be applied to obtain extended cDNAs for any 5' EST in the NetGene™ database, including those 5' ESTs encoding secreted proteins. The method is summarized in figure 6.

1. Obtaining Extended cDNAs

a) First strand synthesis

The method takes advantage of the known 5' sequence of the mRNA. A reverse transcription reaction is conducted on purified mRNA with a poly 14dT primer containing a 49 nucleotide sequence at its 5' end allowing the addition of a known sequence at the end of the cDNA which corresponds to the 3' end of

the mRNA. For example, the primer may have the following sequence: 5'-ATC GTT GAG ACT CGT ACC AGC AGA GTC ACG AGA GAG ACT ACA CGG TAC TGG TTT TTT TTT TTT TTVN -3' (SEQ ID NO:14). Those skilled in the art will appreciate that other sequences may also be added to the poly dT sequence and used to prime the first strand synthesis. Using this primer and a reverse transcriptase such as the Superscript II (Gibco BRL) or Rnase H Minus M-MLV (Promega) enzyme, a reverse transcript anchored at the 3' polyA site of the RNAs is generated.

After removal of the mRNA hybridized to the first cDNA strand by alkaline hydrolysis, the products of the alkaline hydrolysis and the residual poly dT primer are eliminated with an exclusion column such as an AcA34 (Biosepra) matrix as explained in Example 11.

b) Second strand synthesis

A pair of nested primers on each end is designed based on the known 5' sequence from the 5' EST and the known 3' end added by the poly dT primer used in the first strand synthesis. Softwares used to design primers are either based on GC content and melting temperatures of oligonucleotides, such as OSP (Illier and Green, *PCR Meth. Appl.* 1:124-128, 1991), or based on the octamer frequency disparity method (Griffais et al., *Nucleic Acids Res.* 19: 3887-3891, 1991 such as PC-Rare (<http://bioinformatics.weizmann.ac.il/software/PC-Rare/doc/manuel.html>)).

Preferably, the nested primers at the 5' end are separated from one another by four to nine bases. The 5' primer sequences may be selected to have melting temperatures and specificities suitable for use in PCR.

Preferably, the nested primers at the 3' end are separated from one another by four to nine bases. For example, the nested 3' primers may have the following sequences: (5'- CCA GCA GAG TCA CGA GAG AGA CTA CAC GG -3'(SEQ ID NO:15), and 5'- CAC GAG AGA GAC TAC ACG GTA CTG G -3' (SEQ ID NO:16). These primers were selected because they have melting temperatures and specificities compatible with their use in PCR. However, those skilled in the art will appreciate that other sequences may also be used as primers.

The first PCR run of 25 cycles is performed using the Advantage Tth Polymerase Mix (Clontech) and the outer primer from each of the nested pairs. A second 20 cycle PCR using the same enzyme and the inner primer from each of the nested pairs is then performed on 1/2500 of the first PCR product. Thereafter, the primers and nucleotides are removed.

2. Sequencing of Full Length Extended cDNAs or Fragments Thereof

Due to the lack of position constraints on the design of 5' nested primers compatible for PCR use using the OSP software, amplicons of two types are obtained. Preferably, the second 5' primer is located upstream of the translation initiation codon thus yielding a nested PCR product containing the whole coding sequence. Such a full length extended cDNA undergoes a direct cloning procedure as described in section a. However, in some cases, the second 5' primer is located downstream of the translation initiation codon, thereby yielding a PCR product containing only part of the ORF. Such incomplete PCR products are

submitted to a modified procedure described in section b.

a) Nested PCR products containing complete ORFs

When the resulting nested PCR product contains the complete coding sequence, as predicted from the 5'EST sequence, it is cloned in an appropriate vector such as pED6dpc2, as described in section 3.

5 b) Nested PCR products containing incomplete ORFs

When the amplicon does not contain the complete coding sequence, intermediate steps are necessary to obtain both the complete coding sequence and a PCR product containing the full coding sequence. The complete coding sequence can be assembled from several partial sequences determined directly from different PCR products as described in the following section.

10 Once the full coding sequence has been completely determined, new primers compatible for PCR use are designed to obtain amplicons containing the whole coding region. However, in such cases, 3' primers compatible for PCR use are located inside the 3' UTR of the corresponding mRNA, thus yielding amplicons which lack part of this region, i.e. the polyA tract and sometimes the polyadenylation signal, as illustrated in figure 6. Such full length extended cDNAs are then cloned into an appropriate vector as described in section 3.

c) Sequencing extended cDNAs

Sequencing of extended cDNAs is performed using a Die Terminator approach with the AmpliTaq DNA polymerase FS kit available from Perkin Elmer.

15 In order to sequence PCR fragments, primer walking is performed using software such as OSP to choose primers and automated computer software such as ASMG (Sutton et al., *Genome Science Technol.* 1: 9-19, 1995) to construct contigs of walking sequences including the initial 5' tag using minimum overlaps of 32 nucleotides. Preferably, primer walking is performed until the sequences of full length cDNAs are obtained.

25 Completion of the sequencing of a given extended cDNA fragment is assessed as follows. Since sequences located after a polyA tract are difficult to determine precisely in the case of uncloned products, sequencing and primer walking processes for PCR products are interrupted when a polyA tract is identified in extended cDNAs obtained as described in case b. The sequence length is compared to the size of the nested PCR product obtained as described above. Due to the limited accuracy of the determination of the PCR product size by gel electrophoresis, a sequence is considered complete if the size of the obtained
30 sequence is at least 70 % the size of the first nested PCR product. If the length of the sequence determined from the computer analysis is not at least 70% of the length of the nested PCR product, these PCR products are cloned and the sequence of the insertion is determined. When Northern blot data are available, the size of the mRNA detected for a given PCR product is used to finally assess that the sequence is complete. Sequences which do not fulfill the above criteria are discarded and will undergo a new isolation procedure.

35 Sequence data of all extended cDNAs are then transferred to a proprietary database, where quality controls and validation steps are carried out as described in example 15.

3. Cloning of Full Length Extended cDNAs

The PCR product containing the full coding sequence is then cloned in an appropriate vector. For example, the extended cDNAs can be cloned into the expression vector pED6dpc2 (DiscoverEase, Genetics Institute, Cambridge, MA) as follows. The structure of pED6dpc2 is shown in Figure 7. pED6dpc2 vector DNA is prepared with blunt ends by performing an EcoRI digestion followed by a fill in reaction. The blunt ended vector is dephosphorylated. After removal of PCR primers and ethanol precipitation, the PCR product containing the full coding sequence or the extended cDNA obtained as described above is phosphorylated with a kinase subsequently removed by phenol-Sevag extraction and precipitation. The double stranded extended cDNA is then ligated to the vector and the resulting expression plasmid introduced into appropriate host cells.

Since the PCR products obtained as described above are blunt ended molecules that can be cloned in either direction, the orientation of several clones for each PCR product is determined. Then, 4 to 10 clones are ordered in microtiter plates and subjected to a PCR reaction using a first primer located in the vector close to the cloning site and a second primer located in the portion of the extended cDNA corresponding to the 3' end of the mRNA. This second primer may be the antisense primer used in anchored PCR in the case of direct cloning (case a) or the antisense primer located inside the 3'UTR in the case of indirect cloning (case b). Clones in which the start codon of the extended cDNA is operably linked to the promoter in the vector so as to permit expression of the protein encoded by the extended cDNA are conserved and sequenced. In addition to the ends of cDNA inserts, approximately 50 bp of vector DNA on each side of the cDNA insert are also sequenced.

The cloned PCR products are then entirely sequenced according to the aforementioned procedure. In this case, contig assembly of long fragments is then performed on walking sequences that have already contiguated for uncloned PCR products during primer walking. Sequencing of cloned amplicons is complete when the resulting contigs include the whole coding region as well as overlapping sequences with vector DNA on both ends.

4. Computer Analysis of Full Length Extended cDNA

Sequences of all full length extended cDNAs are then submitted to further analysis as described below and using the parameters found in Table I with the following modifications. For screening of miscellaneous subdivisions of Genbank, FASTA was used instead of BLASTN and 15 nucleotide of homology was the limit instead of 17. For Alu detection, BLASTN was used with the following parameters: S=72; identity=70%; and length = 40 nucleotides. Polyadenylation signal and polyA tail which were not search for the 5' ESTs were searched. For polyadenylation signal detection the signal (AATAAA) was searched with one permissible mismatch in the last ten nucleotides preceding the 5' end of the polyA. For the polyA, a stretch of 8 amino acids in the last 20 nucleotides of the sequence was searched with BLAST2N in the sense strand with the following parameters (W=6, S=10, E=1000, and identity=90%). Finally, patented sequences and ORF homologies were searched using, respectively, BLASTN and

BLASTP on GenSEQ (Derwent's database of patented nucleotide sequences) and SWISSPROT for ORFs with the following parameters (W=8 and B=10). Before examining the extended full length cDNAs for sequences of interest, extended cDNAs which are not of interest are searched as follows.

a) Elimination of undesired sequences

- 5 Although 5'ESTs were checked to remove contaminants sequences as described in Example 18, a last verification was carried out to identify extended cDNAs sequences derived from undesired sequences such as vector RNAs, transfer RNAs, ribosomal rRNAs, mitochondrial RNAs, prokaryotic RNAs and fungal RNAs using the FASTA and BLASTN programs on both strands of extended cDNAs as described below.

To identify the extended cDNAs encoding vector RNAs, extended cDNAs are compared to the
10 known sequences of vector RNA using the FASTA program. Sequences of extended cDNAs with more than 90% homology over stretches of 15 nucleotides are identified as vector RNA.

To identify the extended cDNAs encoding tRNAs, extended cDNA sequences were compared to the sequences of 1190 known tRNAs obtained from EMBL release 38, of which 100 were human.
15 Sequences of extended cDNAs having more than 80% homology over 60 nucleotides using FASTA were identified as tRNA.

To identify the extended cDNAs encoding rRNAs, extended cDNA sequences were compared to the sequences of 2497 known rRNAs obtained from EMBL release 38, of which 73 were human.
20 Sequences of extended cDNAs having more than 80% homology over stretches longer than 40 nucleotides using BLASTN were identified as rRNAs.

To identify the extended cDNAs encoding mtRNAs, extended cDNA sequences were compared to the sequences of the two known mitochondrial genomes for which the entire genomic sequences are available and all sequences transcribed from these mitochondrial genomes including tRNAs, rRNAs, and mRNAs for a total of 38 sequences. Sequences of extended cDNAs having more than 80% homology over stretches longer than 40 nucleotides using BLASTN were identified as mtRNAs.

25 Sequences which might have resulted from other exogenous contaminants were identified by comparing extended cDNA sequences to release 105 of Genbank bacterial and fungal divisions. Sequences of extended cDNAs having more than 90% homology over 40 nucleotides using BLASTN were identified as exogenous prokaryotic or fungal contaminants.

In addition, extended cDNAs were searched for different repeat sequences, including Alu
30 sequences, L1 sequences, THE and MER repeats, SSTR sequences or satellite, micro-satellite, or telomeric repeats. Sequences of extended cDNAs with more than 70% homology over 40 nucleotide stretches using BLASTN were identified as repeat sequences and masked in further identification procedures. In addition, clones showing extensive homology to repeats, i.e., matches of either more than 50 nucleotides if the homology was at least 75% or more than 40 nucleotides if the homology was at least
35 85% or more than 30 nucleotides if the homology was at least 90%, were flagged.

b) Identification of structural features

Structural features, e.g. polyA tail and polyadenylation signal, of the sequences of full length extended cDNAs are subsequently determined as follows.

A polyA tail is defined as a homopolymeric stretch of at least 11 A with at most one alternative base within it. The polyA tail search is restricted to the last 20 nt of the sequence and limited to stretches of 11 consecutive A's because sequencing reactions are often not readable after such a polyA stretch. Stretches with 100% homology over 6 nucleotides are identified as polyA tails.

To search for a polyadenylation signal, the polyA tail is clipped from the full-length sequence. The 50 bp preceding the polyA tail are searched for the canonic polyadenylation AAUAAA signal allowing one mismatch to account for possible sequencing errors and known variation in the canonical sequence of the polyadenylation signal.

c) Identification of functional features

Functional features, e.g. ORFs and signal sequences, of the sequences of full length extended cDNAs were subsequently determined as follows.

The 3 upper strand frames of extended cDNAs are searched for ORFs defined as the maximum length fragments beginning with a translation initiation codon and ending with a stop codon. ORFs encoding at least 20 amino acids are preferred.

Each found ORF is then scanned for the presence of a signal peptide in the first 50 amino-acids or, where appropriate, within shorter regions down to 20 amino acids or less in the ORF, using the matrix method of von Heijne (Nuc. Acids Res. **14**: 4683-4690 (1986)), the disclosure of which is incorporated herein by reference and the modification described in Example 22.

d) Homology to either nucleotidic or proteic sequences

Sequences of full length extended cDNAs are then compared to known sequences on a nucleotidic or proteic basis.

Sequences of full length extended cDNAs are compared to the following known nucleic acid sequences: vertebrate sequences (Genbank release # GB), EST sequences (Genbank release # GB), patented sequences (Genseqn release GSEQ) and recently identified sequences (Genbank daily release) available at the time of filing. Full length cDNA sequences are also compared to the sequences of a private database (Genset internal sequences) in order to find sequences that have already been identified by applicants. Sequences of full length extended cDNAs with more than 90% homology over 30 nucleotides using either BLASTN or BLAST2N as indicated in Table II are identified as sequences that have already been described. Matching vertebrate sequences are subsequently examined using FASTA; full length extended cDNAs with more than 70% homology over 30 nucleotides are identified as sequences that have already been described.

ORFs encoded by full length extended cDNAs as defined in section c) are subsequently compared to known amino acid sequences found in Swissprot release CHP, PIR release PIR# and Genpept release GPEPT public databases using BLASTP with the parameter W=8 and allowing a maximum of 10 matches.

Sequences of full length extended cDNAs showing extensive homology to known protein sequences are recognized as already identified proteins.

In addition, the three-frame conceptual translation products of the top strand of full length extended cDNAs are compared to publicly known amino acid sequences of Swissprot using BLASTX with the parameter $E=0.001$. Sequences of full length extended cDNAs with more than 70% homology over 30 amino acid stretches are detected as already identified proteins.

5. Selection of Cloned Full Length Sequences of the Present Invention

Cloned full length extended cDNA sequences that have already been characterized by the aforementioned computer analysis are then submitted to an automatic procedure in order to preselect full length extended cDNAs containing sequences of interest.

a) Automatic sequence preselection

All complete cloned full length extended cDNAs clipped for vector on both ends are considered. First, a negative selection is operated in order to eliminate unwanted cloned sequences resulting from either contaminants or PCR artifacts as follows. Sequences matching contaminant sequences such as vector RNA, tRNA, mtRNA, rRNA sequences are discarded as well as those encoding ORF sequences exhibiting extensive homology to repeats as defined in section 4 a). Sequences obtained by direct cloning using nested primers on 5' and 3' tags (section 1. case a) but lacking polyA tail are discarded. Only ORFs containing a signal peptide and ending either before the polyA tail (case a) or before the end of the cloned 3'UTR (case b) are kept. Then, ORFs containing unlikely mature proteins such as mature proteins which size is less than 20 amino acids or less than 25% of the immature protein size are eliminated.

In the selection of the OFR, priority was given to the ORF and the frame corresponding to the polypeptides described in SignalTag Patents (United States Patent Application Serial Nos: 08/905,223; 08/905,135; 08/905,051; 08/905,144; 08/905,279; 08/904,468; 08/905,134; and 08/905,133). If the ORF was not found among the OFRs described in the SignalTag Patents, the ORF encoding the signal peptide with the highest score according to Von Heijne method as defined in Example 22 was chosen. If the scores were identical, then the longest ORF was chosen.

Sequences of full length extended cDNA clones are then compared pairwise with BLAST after masking of the repeat sequences. Sequences containing at least 90% homology over 30 nucleotides are clustered in the same class. Each cluster is then subjected to a cluster analysis that detects sequences resulting from internal priming or from alternative splicing, identical sequences or sequences with several frameshifts. This automatic analysis serves as a basis for manual selection of the sequences.

b) Manual sequence selection

Manual selection is carried out using automatically generated reports for each sequenced full length extended cDNA clone. During this manual procedures, a selection is operated between clones belonging to the same class as follows. ORF sequences encoded by clones belonging to the same class are aligned and compared. If the homology between nucleotidic sequences of clones belonging to the same class is more

than 90% over 30 nucleotide stretches or if the homology between amino acid sequences of clones belonging to the same class is more than 80% over 20 amino acid stretches, than the clones are considered as being identical. The chosen ORF is the best one according to the criteria mentioned below. If the nucleotide and amino acid homologies are less than 90% and 80% respectively, the clones are said to encode distinct proteins which can be both selected if they contain sequences of interest.

Selection of full length extended cDNA clones encoding sequences of interest is performed using the following criteria. Structural parameters (initial tag, polyadenylation site and signal) are first checked. Then, homologies with known nucleic acids and proteins are examined in order to determine whether the clone sequence match a known nucleic/proteic sequence and, in the latter case, its covering rate and the date at which the sequence became public. If there is no extensive match with sequences other than ESTs or genomic DNA, or if the clone sequence brings substantial new information, such as encoding a protein resulting from alternative slicing of an mRNA coding for an already known protein, the sequence is kept. Examples of such cloned full length extended cDNAs containing sequences of interest are described in Example 28. Sequences resulting from chimera or double inserts as assessed by homology to other sequences are discarded during this procedure.

EXAMPLE 28

Cloning and Sequencing of Extended cDNAs

The procedure described in Example 27 above was used to obtain the extended cDNAs of the present invention. Using this approach, the full length cDNA of SEQ ID NO:17 was obtained. This cDNA falls into the "EST-ext" category described above and encodes the signal peptide MKKVLLLITAILAVAVG (SEQ ID NO: 18) having a von Heijne score of 8.2.

The full length cDNA of SEQ ID NO:49 was also obtained using this procedure. This cDNA falls into the "EST-ext" category described above and encodes the signal peptide MWWFQQGLSFLPSALVIWTS (SEQ ID NO:20) having a von Heijne score of 5.5.

Another full length cDNA obtained using the procedure described above has the sequence of SEQ ID NO:21. This cDNA, falls into the "EST-ext" category described above and encodes the signal peptide MVLTTLPANSANSPVNMPTTGPNLSYASSALSPCLT (SEQ ID NO:22) having a von Heijne score of 5.9.

The above procedure was also used to obtain a full length cDNA having the sequence of SEQ ID NO:23. This cDNA falls into the "EST-ext" category described above and encodes the signal peptide ILSTVTALTFA (SEQ ID NO:24) having a von Heijne score of 5.5.

The full length cDNA of SEQ ID NO:25 was also obtained using this procedure. This cDNA falls into the "new" category described above and encodes a signal peptide LVLTLCTLPLAVA (SEQ ID NO:26) having a von Heijne score of 10.1.

The full length cDNA of SEQ ID NO:27 was also obtained using this procedure. This cDNA falls

into the "new" category described above and encodes a signal peptide LWLLFFLVTAIHA (SEQ ID NO:28) having a von Heijne score of 10.7.

The above procedures were also used to obtain the extended cDNAs of the present invention. 5' ESTs expressed in a variety of tissues were obtained as described above. The appended sequence listing provides the tissues from which the extended cDNAs were obtained. It will be appreciated that the extended cDNAs may also be expressed in tissues other than the tissue listed in the sequence listing.

5' ESTs obtained as described above were used to obtain extended cDNAs having the sequences of SEQ ID NOs: 40-86. Table II provides the sequence identification numbers of the extended cDNAs of the present invention, the locations of the full coding sequences in SEQ ID NOs: 40-86 (i.e. the nucleotides encoding both the signal peptide and the mature protein, listed under the heading FCS location in Table II), the locations of the nucleotides in SEQ ID NOs: 40-86 which encode the signal peptides (listed under the heading SigPep Location in Table II), the locations of the nucleotides in SEQ ID NOs: 40-86 which encode the mature proteins generated by cleavage of the signal peptides (listed under the heading Mature Polypeptide Location in Table II), the locations in SEQ ID NOs: 40-86 of stop codons (listed under the heading Stop Codon Location in Table II), the locations in SEQ ID NOs: 40-86 of polyA signals (listed under the heading Poly A Signal Location in Table II) and the locations of polyA sites (listed under the heading Poly A Site Location in Table II).

The polypeptides encoded by the extended cDNAs were screened for the presence of known structural or functional motifs or for the presence of signatures, small amino acid sequences which are well conserved amongst the members of a protein family. The conserved regions have been used to derive consensus patterns or matrices included in the PROSITE data bank, in particular in the file prosite.dat (Release 13.0 of November 1995, located at <http://expasy.hcuge.ch/sprot/prosite.html>). Prosite_convert and prosite_scan programs (http://ulrec3.unil.ch/ftpserveur/prosite_scan) were used to find signatures on the extended cDNAs.

For each pattern obtained with the prosite_convert program from the prosite.dat file, the accuracy of the detection on a new protein sequence has been tested by evaluating the frequency of irrelevant hits on the population of human secreted proteins included in the data bank SWISSPROT. The ratio between the number of hits on shuffled proteins (with a window size of 20 amino acids) and the number of hits on native (unshuffled) proteins was used as an index. Every pattern for which the ration was greater than 20% (one hit on shuffled proteins for 5 hits on native proteins) was skipped during the search with prosite_scan. The program used to shuffle protein sequences (db_shuffled) and the program used to determine the statistics for each pattern in the protein data banks (prosite_statistics) are available on the ftp site http://ulrec3.unil.ch/ftpserveur/prosite_scan.

The results of the search are provided in Table III. The first column provides the ID number of the sequence. The second column indicates the beginning and end positions of the signature. The Prosite definition of the signature is indicated in the third column.

Table IV lists the sequence identification numbers of the polypeptides of SEQ ID NOs: 87-133, the locations of the amino acid residues of SEQ ID NOs: 87-133 in the full length polypeptide (second column), the locations of the amino acid residues of SEQ ID NOs: 87-133 in the signal peptides (third column), and the locations of the amino acid residues of SEQ ID NOs: 87-133 in the mature polypeptide created by cleaving the signal peptide from the full length polypeptide (fourth column). In Table IV, the first amino acid of the signal peptide is designated as amino acid number 1. In the appended sequence listing, the first amino acid of the mature protein resulting from cleavage of the signal peptide is designated as amino acid number 1 and the first amino acid of the signal peptide is designated with the appropriate negative number, in accordance with the regulations governing sequence listings.

The extended cDNAs of the present invention were categorized based on their homology to known sequences. Genebank release #103, division ESTs, and Geneseq release #28 were used to scan the extended cDNAs using Blast. For each extended cDNA ID, the covering rate of the sequence by another sequence was determined as follows. The length in nucleotides of the matching segment was calculated (even when gaps were present) and divided by the length in nucleotides of the extended cDNA sequence. When more than one covering rate was obtained for a given extended cDNA, the higher covering rate was used to classify the extended cDNA. The Geneseq sequences have been categorized as either ESTs or vertebrate, with ESTs being those sequences obtained by random sequencing of cDNA libraries and vertebrate sequences being those sequences containing sequences resembling known functional motifs.

The results of this categorization are provided in Table V. The first column lists the sequence identification number of the sequence being categorized. The second column indicates those sequences having no matches with the database scanned. The third column indicates those sequences having a covering rate of less than 30%. The fourth column indicates those sequences having a covering rate greater than 30%. The fifth column indicates sequences partially or totally covered by vertebrate sequences as described above.

The nucleotide sequences of the sequences of SEQ ID NOs: 40-86 and 134-180, and the amino acid sequences encoded by SEQ ID NOs: 40-86 and 134-180 (i.e. amino acid sequences of SEQ ID NOs: 87-133 and 181-227) are provided in the appended sequence listing. In some instances, the sequences are preliminary and may include some incorrect or ambiguous sequences or amino acids. The sequences of SEQ ID NOs: 40-86 and 134-180 can readily be screened for any errors therein and any sequence ambiguities can be resolved by resequencing a fragment containing such errors or ambiguities on both strands. Nucleic acid fragments for resolving sequencing errors or ambiguities may be obtained from the deposited clones or can be isolated using the techniques described herein. Resolution of any such ambiguities or errors may be facilitated by using primers which hybridize to sequences located close to the ambiguous or erroneous sequences. For example, the primers may hybridize to sequences within 50-75 bases of the ambiguity or error. Upon resolution of an error or ambiguity, the corresponding corrections can be made in the protein sequences encoded by the DNA containing the error or ambiguity. The amino acid sequence of the protein

encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein, and determining its sequence.

For each amino acid sequence, Applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing. Some of the amino acid sequences may contain "Xaa" designators. These "Xaa" designators indicate either (1) a residue which cannot be identified because of nucleotide sequence ambiguity or (2) a stop codon in the determined sequence where Applicants believe one should not exist (if the sequence were determined more accurately).

Cells containing the 47 extended cDNAs (SEQ ID NOs: 134-180) of the present invention in the vector pED6dpc2, are maintained in permanent deposit by the inventors at Genset, S.A., 24 Rue Royale, 75008 Paris, France.

A pool of the cells containing the 47 extended cDNAs (SEQ ID NOs: 134-180), from which the cells containing a particular polynucleotide is obtainable, will be deposited with the American Type Culture Collection. Each extended cDNA clone will be transfected into separate bacterial cells (E-coli) in this composite deposit. A pool of cells containing the 43 extended cDNAs (SEQ ID NOs: 134, 136-143, 145-162, 164-174, and 176-180), from which the cells containing a particular polynucleotide is obtainable, were deposited with the American Type Culture Collection on December 16, 1997, under the name SignalTag 1-43, and ATCC accession No. 98619. A pool of cells comprising the 2 extended cDNAs (SEQ ID NOs: 144 and 163), from which the cells containing a particular polynucleotide is obtainable, were deposited with the American Type Culture Collection on October 15, 1998, under the name SignalTag 44-66, and ATCC accession No. 98923. Each extended cDNA can be removed from the pED6dpc2 vector in which it was deposited by performing a NotI, PstI double digestion to produce the appropriate fragment for each clone. The proteins encoded by the extended cDNAs may also be expressed from the promoter in pED6dpc2.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows: An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The design of the oligonucleotide probe should preferably follow these parameters:

(a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;

(b) Preferably, the probe is designed to have a T_m of approx. 80°C (assuming 2 degrees for each A or T and 4 degrees for each G or C). However, probes having melting temperatures between 40 °C and 80 °C may also be used provided that specificity is not lost.

The oligonucleotide should preferably be labeled with $g\text{-}^{32}\text{P}$ ATP (specific activity 6000 Ci/mmmole) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantified by measurement in a scintillation counter. Preferably, specific activity of the resulting

probe should be approximately 4×10^6 dpm/pmole.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 μ l of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 μ g/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 μ g/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 μ g/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1×10^6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the extended cDNA insertion. For example, a PCR reaction may be conducted using a primer having the sequence GGCCATACACTTGAGTGAC (SEQ ID NO:38) and a primer having the sequence ATATAGACAAACGCACACC (SEQ. ID. NO:39). The PCR product which corresponds to the extended cDNA can then be manipulated using standard cloning techniques familiar to those skilled in the art.

In addition to PCR based methods for obtaining extended cDNAs, traditional hybridization based methods may also be employed. These methods may also be used to obtain the genomic DNAs which encode the mRNAs from which the 5' ESTs were derived, mRNAs corresponding to the extended cDNAs, or nucleic acids which are homologous to extended cDNAs or 5' ESTs. Example 29 below provides an example of such methods.

EXAMPLE 29

Methods for Obtaining Extended cDNAs or Nucleic
Acids Homologous to Extended cDNAs or 5' ESTs

A full length cDNA library can be made using the strategies described in Examples 13, 14, 15, and 16 above by replacing the random nonamer used in Example 14 with an oligo-dT primer. For instance, the oligonucleotide of SEQ ID NO:14 may be used.

Alternatively, a cDNA library or genomic DNA library may be obtained from a commercial source or made using techniques familiar to those skilled in the art. The library includes cDNAs which are derived from the mRNA corresponding to a 5' EST or which have homology to an extended cDNA or 5' EST. The cDNA library or genomic DNA library is hybridized to a detectable probe comprising at least 10 consecutive nucleotides from the 5' EST or extended cDNA using conventional techniques. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST or extended cDNA. More preferably, the probe comprises at least 20-30 consecutive nucleotides from the 5' EST or extended cDNA. In some embodiments, the probe comprises more than 30 nucleotides from the 5' EST or extended cDNA.

Techniques for identifying cDNA clones in a cDNA library which hybridize to a given probe sequence are disclosed in Sambrook et al., *Molecular Cloning: A Laboratory Manual* 2d Ed., Cold Spring Harbor Laboratory Press, (1989). The same techniques may be used to isolate genomic DNAs.

Briefly, cDNA or genomic DNA clones which hybridize to the detectable probe are identified and isolated for further manipulation as follows. A probe comprising at least 10 consecutive nucleotides from the 5' EST or extended cDNA is labeled with a detectable label such as a radioisotope or a fluorescent molecule. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST or extended cDNA. More preferably, the probe comprises 20-30 consecutive nucleotides from the 5' EST or extended cDNA. In some embodiments, the probe comprises more than 30 nucleotides from the 5' EST or extended cDNA.

Techniques for labeling the probe are well known and include phosphorylation with polynucleotide kinase, nick translation, in vitro transcription, and non-radioactive techniques. The cDNAs or genomic DNAs in the library are transferred to a nitrocellulose or nylon filter and denatured. After incubation of the filter with a blocking solution, the filter is contacted with the labeled probe and incubated for a sufficient amount of time for the probe to hybridize to cDNAs or genomic DNAs containing a sequence capable of hybridizing to the probe.

By varying the stringency of the hybridization conditions used to identify extended cDNAs or genomic DNAs which hybridize to the detectable probe, extended cDNAs having different levels of homology to the probe can be identified and isolated. To identify extended cDNAs or genomic DNAs having a high degree of homology to the probe sequence, the melting temperature of the probe may be calculated using the following formulas:

For probes between 14 and 70 nucleotides in length the melting temperature (T_m) is calculated using the formula: $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (600/N)$ where N is the length of the probe.

If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (0.63\% \text{ formamide}) - (600/N)$ where N is the length of the probe.

Prehybridization may be carried out in 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 μ g denatured fragmented salmon sperm DNA or 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 μ g denatured fragmented salmon sperm DNA, 50% formamide. The formulas for SSC and Denhardt's solutions are listed in Sambrook et al., supra.

Hybridization is conducted by adding the detectable probe to the prehybridization solutions listed above. Where the probe comprises double stranded DNA, it is denatured before addition to the hybridization solution. The filter is contacted with the hybridization solution for a sufficient period of time to allow the probe to hybridize to extended cDNAs or genomic DNAs containing sequences complementary thereto or homologous thereto. For probes over 200 nucleotides in length, the hybridization may be carried out at 15-25°C below the T_m . For shorter probes, such as oligonucleotide probes, the hybridization may be conducted at 15-25°C below the T_m . Preferably, for hybridizations in 6X SSC, the hybridization is conducted at approximately 68°C. Preferably, for hybridizations in 50% formamide containing solutions, the hybridization is conducted at approximately 42°C.

All of the foregoing hybridizations would be considered to be under "stringent" conditions. Following hybridization, the filter is washed in 2X SSC, 0.1% SDS at room temperature for 15 minutes. The filter is then washed with 0.1X SSC, 0.5% SDS at room temperature for 30 minutes to 1 hour. Thereafter, the solution is washed at the hybridization temperature in 0.1X SSC, 0.5% SDS. A final wash is conducted in 0.1X SSC at room temperature.

Extended cDNAs, nucleic acids homologous to extended cDNAs or 5' ESTs, or genomic DNAs which have hybridized to the probe are identified by autoradiography or other conventional techniques.

The above procedure may be modified to identify extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs having decreasing levels of homology to the probe sequence. For example, to obtain extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs of decreasing homology to the detectable probe, less stringent conditions may be used. For example, the hybridization temperature may be decreased in increments of 5°C from 68°C to 42°C in a hybridization buffer having a Na^+ concentration of approximately 1M. Following hybridization, the filter may be washed with 2X SSC, 0.5% SDS at the temperature of hybridization. These conditions are considered to be "moderate" conditions above 50°C and "low" conditions below 50°C.

Alternatively, the hybridization may be carried out in buffers, such as 6X SSC, containing formamide at a temperature of 42°C. In this case, the concentration of formamide in the hybridization

buffer may be reduced in 5% increments from 50% to 0% to identify clones having decreasing levels of homology to the probe. Following hybridization, the filter may be washed with 6X SSC, 0.5% SDS at 50°C. These conditions are considered to be "moderate" conditions above 25% formamide and "low" conditions below 25% formamide.

5 Extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs which have hybridized to the probe are identified by autoradiography.

If it is desired to obtain nucleic acids homologous to extended cDNAs, such as allelic variants thereof or nucleic acids encoding proteins related to the proteins encoded by the extended cDNAs, the level of homology between the hybridized nucleic acid and the extended cDNA or 5' EST used as the probe may readily be determined. To determine the level of homology between the hybridized nucleic acid and the extended cDNA or 5' EST from which the probe was derived, the nucleotide sequences of the hybridized nucleic acid and the extended cDNA or 5' EST from which the probe was derived are compared. For example, using the above methods, nucleic acids having at least 95% nucleic acid homology to the extended cDNA or 5' EST from which the probe was derived may be obtained and identified. Similarly, by using progressively less stringent hybridization conditions one can obtain and identify nucleic acids having at least 90%, at least 85%, at least 80% or at least 75% homology to the extended cDNA or 5' EST from which the probe was derived.

To determine whether a clone encodes a protein having a given amount of homology to the protein encoded by the extended cDNA or 5' EST, the amino acid sequence encoded by the extended cDNA or 5' EST is compared to the amino acid sequence encoded by the hybridizing nucleic acid. Homology is determined to exist when an amino acid sequence in the extended cDNA or 5' EST is closely related to an amino acid sequence in the hybridizing nucleic acid. A sequence is closely related when it is identical to that of the extended cDNA or 5' EST or when it contains one or more amino acid substitutions therein in which amino acids having similar characteristics have been substituted for one another. Using the above methods, one can obtain nucleic acids encoding proteins having at least 95%, at least 90%, at least 85%, at least 80% or at least 75% homology to the proteins encoded by the extended cDNA or 5' EST from which the probe was derived.

Alternatively, extended cDNAs may be prepared by obtaining mRNA from the tissue, cell, or organism of interest using mRNA preparation procedures utilizing poly A selection procedures or other techniques known to those skilled in the art. A first primer capable of hybridizing to the poly A tail of the mRNA is hybridized to the mRNA and a reverse transcription reaction is performed to generate a first cDNA strand.

The first cDNA strand is hybridized to a second primer containing at least 10 consecutive nucleotides of the sequences of the 5' EST for which an extended cDNA is desired. Preferably, the primer comprises at least 12, 15, or 17 consecutive nucleotides from the sequences of the 5' EST. More preferably, the primer comprises 20-30 consecutive nucleotides from the sequences of the 5' EST. In some

embodiments, the primer comprises more than 30 nucleotides from the sequences of the 5' EST. If it is desired to obtain extended cDNAs containing the full protein coding sequence, including the authentic translation initiation site, the second primer used contains sequences located upstream of the translation initiation site. The second primer is extended to generate a second cDNA strand complementary to the first cDNA strand. Alternatively, RTPCR may be performed as described above using primers from both ends of the cDNA to be obtained.

Extended cDNAs containing 5' fragments of the mRNA may be prepared by contacting an mRNA comprising the sequence of the 5' EST for which an extended cDNA is desired with a primer comprising at least 10 consecutive nucleotides of the sequences complementary to the 5' EST, hybridizing the primer to the mRNAs, and reverse transcribing the hybridized primer to make a first cDNA strand from the mRNAs. Preferably, the primer comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST. More preferably, the primer comprises 20-30 consecutive nucleotides from the 5' EST.

Thereafter, a second cDNA strand complementary to the first cDNA strand is synthesized. The second cDNA strand may be made by hybridizing a primer complementary to sequences in the first cDNA strand to the first cDNA strand and extending the primer to generate the second cDNA strand.

The double stranded extended cDNAs made using the methods described above are isolated and cloned. The extended cDNAs may be cloned into vectors such as plasmids or viral vectors capable of replicating in an appropriate host cell. For example, the host cell may be a bacterial, mammalian, avian, or insect cell.

Techniques for isolating mRNA, reverse transcribing a primer hybridized to mRNA to generate a first cDNA strand, extending a primer to make a second cDNA strand complementary to the first cDNA strand, isolating the double stranded cDNA and cloning the double stranded cDNA are well known to those skilled in the art and are described in Current Protocols in Molecular Biology, John Wiley 503 Sons, Inc. (1997); and Sambrook et al. *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, (1989).

Alternatively, kits for obtaining full length cDNAs, such as the GeneTrapper (Cat. No. 10356-020, Gibco, BRL), may be used for obtaining full length cDNAs or extended cDNAs. In this approach, full length or extended cDNAs are prepared from mRNA and cloned into double stranded phagemids. The cDNA library in the double stranded phagemids is then rendered single stranded by treatment with an endonuclease, such as the Gene II product of the phage F1, and Exonuclease III as described in the manual accompanying the GeneTrapper kit. A biotinylated oligonucleotide comprising the sequence of a 5' EST, or a fragment containing at least 10 nucleotides thereof, is hybridized to the single stranded phagemids. Preferably, the fragment comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST. More preferably, the fragment comprises 20-30 consecutive nucleotides from the 5' EST. In some procedures, the fragment may comprise more than 30 consecutive nucleotides from the 5' EST.

Hybrids between the biotinylated oligonucleotide and phagemids having inserts containing the 5'

EST sequence are isolated by incubating the hybrids with streptavidin coated paramagnetic beads and retrieving the beads with a magnet. Thereafter, the resulting phagemids containing the 5' EST sequence are released from the beads and converted into double stranded DNA using a primer specific for the 5' EST sequence. The resulting double stranded DNA is transformed into bacteria. Extended cDNAs containing the 5' EST sequence are identified by colony PCR or colony hybridization.

A plurality of extended cDNAs containing full length protein coding sequences or sequences encoding only the mature protein remaining after the signal peptide is cleaved may be provided as cDNA libraries for subsequent evaluation of the encoded proteins or use in diagnostic assays as described below.

IV. Expression of Proteins Encoded by Extended cDNAs Isolated Using 5' ESTs

Extended cDNAs containing the full protein coding sequences of their corresponding mRNAs or portions thereof, such as cDNAs encoding the mature protein, may be used to express the secreted proteins or portions thereof which they encode as described in Example 30 below. If desired, the extended cDNAs may contain the sequences encoding the signal peptide to facilitate secretion of the expressed protein. It will be appreciated that a plurality of extended cDNAs containing the full protein coding sequences or portions thereof may be simultaneously cloned into expression vectors to create an expression library for analysis of the encoded proteins as described below.

EXAMPLE 30

Expression of the Proteins Encoded by Extended cDNAs or Portions Thereof

To express the proteins encoded by the extended cDNAs or portions thereof, nucleic acids containing the coding sequence for the proteins or portions thereof to be expressed are obtained as described in Examples 27-29 and cloned into a suitable expression vector. If desired, the nucleic acids may contain the sequences encoding the signal peptide to facilitate secretion of the expressed protein. For example, the nucleic acid may comprise the sequence of one of SEQ ID NOs: 134-180 listed in Table VII and in the accompanying sequence listing. Alternatively, the nucleic acid may comprise those nucleotides which make up the full coding sequence of one of the sequences of SEQ ID NOs: 134-180 as defined in Table VII above.

It will be appreciated that should the extent of the full coding sequence (i.e. the sequence encoding the signal peptide and the mature protein resulting from cleavage of the signal peptide) differ from that listed in Table VII as a result of a sequencing error, reverse transcription or amplification error, mRNA splicing, post-translational modification of the encoded protein, enzymatic cleavage of the encoded protein, or other biological factors, one skilled in the art would be readily able to identify the extent of the full coding sequences in the sequences of SEQ ID NOs. 134-180. Accordingly, the scope of any claims herein relating to nucleic acids containing the full coding sequence of one of SEQ ID NOs. 134-180 is not to be construed as excluding any readily identifiable variations from or equivalents to the full coding sequences listed in Table VII. Similarly, should the extent of the full length polypeptides differ from those indicated in Table VIII as a result of any of the preceding factors, the scope of claims relating to polypeptides

comprising the amino acid sequence of the full length polypeptides is not to be construed as excluding any readily identifiable variations from or equivalents to the sequences listed in Table VIII.

Alternatively, the nucleic acid used to express the protein or portion thereof may comprise those nucleotides which encode the mature protein (i.e. the protein created by cleaving the signal peptide off) encoded by one of the sequences of SEQ ID NOs: 134-180 as defined in Table VII.

It will be appreciated that should the extent of the sequence encoding the mature protein differ from that listed in Table VII as a result of a sequencing error, reverse transcription or amplification error, mRNA splicing, post-translational modification of the encoded protein, enzymatic cleavage of the encoded protein, or other biological factors, one skilled in the art would be readily able to identify the extent of the sequence encoding the mature protein in the sequences of SEQ ID NOs: 134-180. Accordingly, the scope of any claims herein relating to nucleic acids containing the sequence encoding the mature protein encoded by one of SEQ ID NOs: 134-180 is not to be construed as excluding any readily identifiable variations from or equivalents to the sequences listed in Table VII. Thus, claims relating to nucleic acids containing the sequence encoding the mature protein encompass equivalents to the sequences listed in Table VII, such as sequences encoding biologically active proteins resulting from post-translational modification, enzymatic cleavage, or other readily identifiable variations from or equivalents to the proteins in addition to cleavage of the signal peptide. Similarly, should the extent of the mature polypeptides differ from those indicated in Table VIII as a result of any of the preceding factors, the scope of claims relating to polypeptides comprising the sequence of a mature protein included in the sequence of one of SEQ ID NOs. 181-227 is not to be construed as excluding any readily identifiable variations from or equivalents to the sequences listed in Table VIII. Thus, claims relating to polypeptides comprising the sequence of the mature protein encompass equivalents to the sequences listed in Table VIII, such as biologically active proteins resulting from post-translational modification, enzymatic cleavage, or other readily identifiable variations from or equivalents to the proteins in addition to cleavage of the signal peptide. It will also be appreciated that should the biologically active form of the polypeptides included in the sequence of one of SEQ ID NOs. 181-227 or the nucleic acids encoding the biologically active form of the polypeptides differ from those identified as the mature polypeptide in Table VIII or the nucleotides encoding the mature polypeptide in Table VII as a result of a sequencing error, reverse transcription or amplification error, mRNA splicing, post-translational modification of the encoded protein, enzymatic cleavage of the encoded protein, or other biological factors, one skilled in the art would be readily able to identify the amino acids in the biologically active form of the polypeptides and the nucleic acids encoding the biologically active form of the polypeptides. In such instances, the claims relating to polypeptides comprising the mature protein included in one of SEQ ID NOs. 181-227 or nucleic acids comprising the nucleotides of one of SEQ ID NOs. 134-180 encoding the mature protein shall not be construed to exclude any readily identifiable variations from the sequences listed in Table VII and Table VIII.

In some embodiments, the nucleic acid used to express the protein or portion thereof may comprise

those nucleotides which encode the signal peptide encoded by one of the sequences of SEQ ID NOs: 134-180 as defined in Table VII above.

It will be appreciated that should the extent of the sequence encoding the signal peptide differ from that listed in Table VII as a result of a sequencing error, reverse transcription or amplification error, mRNA splicing, post-translational modification of the encoded protein, enzymatic cleavage of the encoded protein, or other biological factors, one skilled in the art would be readily able to identify the extent of the sequence encoding the signal peptide in the sequences of SEQ ID NOs. 134-180. Accordingly, the scope of any claims herein relating to nucleic acids containing the sequence encoding the signal peptide encoded by one of SEQ ID NOs.134-180 is not to be construed as excluding any readily identifiable variations from the sequences listed in Table VII. Similarly, should the extent of the signal peptides differ from those indicated in Table VIII as a result of any of the preceding factors, the scope of claims relating to polypeptides comprising the sequence of a signal peptide included in the sequence of one of SEQ ID NOs. 181-227 is not to be construed as excluding any readily identifiable variations from the sequences listed in Table VIII.

Alternatively, the nucleic acid may encode a polypeptide comprising at least 10 consecutive amino acids of one of the sequences of SEQ ID NOs: 181-227. In some embodiments, the nucleic acid may encode a polypeptide comprising at least 15 consecutive amino acids of one of the sequences of SEQ ID NOs: 181-227. In other embodiments, the nucleic acid may encode a polypeptide comprising at least 25 consecutive amino acids of one of the sequences of SEQ ID NOs: 181-227.

The nucleic acids inserted into the expression vectors may also contain sequences upstream of the sequences encoding the signal peptide, such as sequences which regulate expression levels or sequences which confer tissue specific expression.

The nucleic acid encoding the protein or polypeptide to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The expression vector may be any of the mammalian, yeast, insect or bacterial expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, et al., U.S. Patent No. 5,082,767.

The following is provided as one exemplary method to express the proteins encoded by the extended cDNAs corresponding to the 5' ESTs or the nucleic acids described above. First, the methionine initiation codon for the gene and the poly A signal of the gene are identified. If the nucleic acid encoding the polypeptide to be expressed lacks a methionine to serve as the initiation site, an initiating methionine can be introduced next to the first codon of the nucleic acid using conventional techniques. Similarly, if the extended cDNA lacks a poly A signal, this sequence can be added to the construct by, for example, splicing out the Poly A signal from pSG5 (Stratagene) using BglII and SalI restriction endonuclease enzymes and

incorporating it into the mammalian expression vector pXT1 (Stratagene). pXT1 contains the LTRs and a portion of the *gag* gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex Thymidine Kinase promoter and the selectable neomycin gene. The extended cDNA or portion thereof encoding the polypeptide to be expressed is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the extended cDNA or portion thereof and containing restriction endonuclease sequences for Pst I incorporated into the 5' primer and BglII at the 5' end of the corresponding cDNA 3' primer, taking care to ensure that the extended cDNA is positioned in frame with the poly A signal. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with Bgl II, purified and ligated to pXT1, now containing a poly A signal and digested with BglII.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600ug/ml G418 (Sigma, St. Louis, Missouri). Preferably the expressed protein is released into the culture medium, thereby facilitating purification.

Alternatively, the extended cDNAs may be cloned into pED6dpc2 as described above. The resulting pED6dpc2 constructs may be transfected into a suitable host cell, such as COS 1 cells. Methotrexate resistant cells are selected and expanded. Preferably, the protein expressed from the extended cDNA is released into the culture medium thereby facilitating purification.

Proteins in the culture medium are separated by gel electrophoresis. If desired, the proteins may be ammonium sulfate precipitated or separated based on size or charge prior to electrophoresis.

As a control, the expression vector lacking a cDNA insert is introduced into host cells or organisms and the proteins in the medium are harvested. The secreted proteins present in the medium are detected using techniques such as Coomassie or silver staining or using antibodies against the protein encoded by the extended cDNA. Coomassie and silver staining techniques are familiar to those skilled in the art.

Antibodies capable of specifically recognizing the protein of interest may be generated using synthetic 15-mer peptides having a sequence encoded by the appropriate 5' EST, extended cDNA, or portion thereof. The synthetic peptides are injected into mice to generate antibody to the polypeptide encoded by the 5' EST, extended cDNA, or portion thereof.

Secreted proteins from the host cells or organisms containing an expression vector which contains the extended cDNA derived from a 5' EST or a portion thereof are compared to those from the control cells or organism. The presence of a band in the medium from the cells containing the expression vector which is absent in the medium from the control cells indicates that the extended cDNA encodes a secreted protein. Generally, the band corresponding to the protein encoded by the extended cDNA will have a mobility near that expected based on the number of amino acids in the open reading frame of the extended cDNA.

However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

Alternatively, if the protein expressed from the above expression vectors does not contain sequences directing its secretion, the proteins expressed from host cells containing an expression vector containing an insert encoding a secreted protein or portion thereof can be compared to the proteins expressed in host cells containing the expression vector without an insert. The presence of a band in samples from cells containing the expression vector with an insert which is absent in samples from cells containing the expression vector without an insert indicates that the desired protein or portion thereof is being expressed. Generally, the band will have the mobility expected for the secreted protein or portion thereof. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

The protein encoded by the extended cDNA may be purified using standard immunochromatography techniques. In such procedures, a solution containing the secreted protein, such as the culture medium or a cell extract, is applied to a column having antibodies against the secreted protein attached to the chromatography matrix. The secreted protein is allowed to bind the immunochromatography column. Thereafter, the column is washed to remove non-specifically bound proteins. The specifically bound secreted protein is then released from the column and recovered using standard techniques.

If antibody production is not possible, the extended cDNA sequence or portion thereof may be incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies the coding sequence of the extended cDNA or portion thereof is inserted in frame with the gene encoding the other half of the chimera. The other half of the chimera may be β -globin or a nickel binding polypeptide encoding sequence. A chromatography matrix having antibody to β -globin or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites may be engineered between the β -globin gene or the nickel binding polypeptide and the extended cDNA or portion thereof. Thus, the two polypeptides of the chimera may be separated from one another by protease digestion.

One useful expression vector for generating β -globin chimerics is pSG5 (Stratagene), which encodes rabbit β -globin. Intron II of the rabbit β -globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques as described are well known to those skilled in the art of molecular biology. Standard methods are published in methods texts such as Davis et al., (*Basic Methods in Molecular Biology*, L.G. Davis, M.D. Dibner, and J.F. Battey, ed., Elsevier Press, NY, 1986) and many of the methods are available from Stratagene, Life Technologies, Inc., or Promega. Polypeptide may additionally be produced from the construct using in vitro translation systems such as the In vitro ExpressTM Translation Kit (Stratagene).

Following expression and purification of the secreted proteins encoded by the 5' ESTs, extended cDNAs, or fragments thereof, the purified proteins may be tested for the ability to bind to the surface of various cell types as described in Example 31 below. It will be appreciated that a plurality of proteins expressed from these cDNAs may be included in a panel of proteins to be simultaneously evaluated for the

activities specifically described below, as well as other biological roles for which assays for determining activity are available.

EXAMPLE 31

Analysis of Secreted Proteins to Determine Whether they Bind to the Cell Surface

The proteins encoded by the 5' ESTs, extended cDNAs, or fragments thereof are cloned into expression vectors such as those described in Example 30. The proteins are purified by size, charge, immunochromatography or other techniques familiar to those skilled in the art. Following purification, the proteins are labeled using techniques known to those skilled in the art. The labeled proteins are incubated with cells or cell lines derived from a variety of organs or tissues to allow the proteins to bind to any receptor present on the cell surface. Following the incubation, the cells are washed to remove non-specifically bound protein. The labeled proteins are detected by autoradiography. Alternatively, unlabeled proteins may be incubated with the cells and detected with antibodies having a detectable label, such as a fluorescent molecule, attached thereto.

Specificity of cell surface binding may be analyzed by conducting a competition analysis in which various amounts of unlabeled protein are incubated along with the labeled protein. The amount of labeled protein bound to the cell surface decreases as the amount of competitive unlabeled protein increases. As a control, various amounts of an unlabeled protein unrelated to the labeled protein is included in some binding reactions. The amount of labeled protein bound to the cell surface does not decrease in binding reactions containing increasing amounts of unrelated unlabeled protein, indicating that the protein encoded by the cDNA binds specifically to the cell surface.

As discussed above, secreted proteins have been shown to have a number of important physiological effects and, consequently, represent a valuable therapeutic resource. The secreted proteins encoded by the extended cDNAs or portions thereof made according to Examples 27-29 may be evaluated to determine their physiological activities as described below.

EXAMPLE 32

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Cytokine, Cell Proliferation or Cell Differentiation Activity

As discussed above, secreted proteins may act as cytokines or may affect cellular proliferation or differentiation. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7c and CMK. The proteins encoded by the above extended cDNAs or portions thereof

may be evaluated for their ability to regulate T cell or thymocyte proliferation in assays such as those described above or in the following references: *Current Protocols in Immunology*, Ed. by J.E. Coligan et al., Greene Publishing Associates and Wiley-Interscience; Takai et al. *J. Immunol.* **137**:3494-3500 (1986); Bertagnolli et al. *J. Immunol.* **145**:1706-1712 (1990); Bertagnolli et al., *Cellular Immunology* **133**:327-341 (1991); Bertagnolli, et al. *J. Immunol.* **149**:3778-3783 (1992); and Bowman et al., *J. Immunol.* **152**:1756-1761 (1994).

In addition, numerous assays for cytokine production and/or the proliferation of spleen cells, lymph node cells and thymocytes are known. These include the techniques disclosed in *Current Protocols in Immunology*. J.E. Coligan et al. Eds., Vol 1 pp. 3.12.1-3.12.14 John Wiley and Sons, Toronto. (1994); and Schreiber, R.D. *Current Protocols in Immunology*, supra Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. (1994).

The proteins encoded by the cDNAs may also be assayed for the ability to regulate the proliferation and differentiation of hematopoietic or lymphopoietic cells. Many assays for such activity are familiar to those skilled in the art, including the assays in the following references: Bottomly, K., Davis, L.S. and Lipsky, P.E., Measurement of Human and Murine Interleukin 2 and Interleukin 4, *Current Protocols in Immunology*, J.E. Coligan et al. Eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. (1991); deVries et al., *J. Exp. Med.* **173**:1205-1211, 1991; Moreau et al., *Nature* **36**:690-692, (1988); Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* **80**:2931-2938, (1983); Nordan, R., Measurement of Mouse and Human Interleukin 6. *Current Protocols in Immunology*. J.E. Coligan et al. Eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. (1991); Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* **83**:1857-1861, 1986; Bennett, F., Giannotti, J., Clark, S.C. and Turner, K.J., Measurement of Human Interleukin 11. *Current Protocols in Immunology*. J.E. Coligan et al. Eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. (1991); and Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J., Measurement of Mouse and Human Interleukin 9. *Current Protocols in Immunology*. J.E. Coligan et al., Eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. (1991).

The proteins encoded by the cDNAs may also be assayed for their ability to regulate T-cell responses to antigens. Many assays for such activity are familiar to those skilled in the art, including the assays described in the following references: Chapter 3 (In Vitro Assays for Mouse Lymphocyte Function), Chapter 6 (Cytokines and Their Cellular Receptors) and Chapter 7, (Immunologic Studies in Humans) *Current Protocols in Immunology*, J.E. Coligan et al. Eds. Greene Publishing Associates and Wiley-Interscience; Weinberger et al., *Proc. Natl. Acad. Sci. USA* **77**:6091-6095 (1980); Weinberger et al., *Eur. J. Immun.* **11**:405-411 (1981); Takai et al., *J. Immunol.* **137**:3494-3500 (1986); and Takai et al., *J. Immunol.* **140**:508-512 (1988).

Those proteins which exhibit cytokine, cell proliferation, or cell differentiation activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which induction of cell proliferation or differentiation is beneficial. Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host

cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 33

Assaying the Proteins Expressed from Extended cDNAs or Portions

Thereof for Activity as Immune System Regulators

The proteins encoded by the cDNAs may also be evaluated for their effects as immune regulators. For example, the proteins may be evaluated for their activity to influence thymocyte or splenocyte cytotoxicity. Numerous assays for such activity are familiar to those skilled in the art including the assays described in the following references: Chapter 3 (In Vitro Assays for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic studies in Humans) *Current Protocols in Immunology*, J.E. Coligan et al. Eds, Greene Publishing Associates and Wiley-Interscience; Herrmann et al., *Proc. Natl. Acad. Sci. USA* **78**:2488-24921 (1981); Herrmann et al., *J. Immunol.* **128**:1968-1974 (1982); Handa et al., *J. Immunol.* **135**:1564-1572 (1985); Takai et al., *J. Immunol.* **137**:3494-3500 (1986); Takai et al., *J. Immunol.* **140**:508-512 (1988); Herrmann et al., *Proc. Natl. Acad. Sci. USA* **78**:2488-2492 (1981); Herrmann et al *J. Immunol.* **128**:1968-1974 (1982); Handa et al., *J. Immunol.* **135**:1564-1572 (1985); Takai et al., *J. Immunol.* **137**:3494-3500 (1986); Bowman et al., *J. Virology* **61**:1992-1998; Takai et al., *J. Immunol.* **140**:508-512 (1988); Bertagnolli et al., *Cellular Immunology* **133**:327-341 (1991); and Brown et al., *J. Immunol.* **153**:3079-3092 (1994).

The proteins encoded by the cDNAs may also be evaluated for their effects on T-cell dependent immunoglobulin responses and isotype switching. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Maliszewski, *J. Immunol.* **144**:3028-3033 (1990); and Mond, J.J. and Brunswick, M. Assays for B Cell Function: *In vitro* Antibody Production, Vol 1 pp. 3.8.1-3.8.16 *Current Protocols in Immunology*. J.E. Coligan et al Eds., John Wiley and Sons, Toronto. (1994).

The proteins encoded by the cDNAs may also be evaluated for their effect on immune effector cells, including their effect on Th1 cells and cytotoxic lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Chapter 3 (In Vitro Assays for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic Studies in Humans) *Current Protocols in Immunology*, J.E. Coligan et al. Eds., Greene Publishing Associates and Wiley-Interscience; Takai et al., *J. Immunol.* **137**:3494-3500 (1986); Takai et al.; *J. Immunol.* **140**:508-512 (1988); and Bertagnolli et al., *J. Immunol.* **149**:3778-3783 (1992).

The proteins encoded by the cDNAs may also be evaluated for their effect on dendritic cell mediated activation of naive T-cells. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Guery et al., *J. Immunol.* **134**:536-544 (1995); Inaba et al., *Journal of Experimental Medicine* **173**:549-559 (1991); Macatonia et al., *J. Immunol.* **154**:5071-5079 (1995); Porgador et al., *Journal of Experimental Medicine* **182**:255-260 (1995); Nair et al.,

Journal of Virology **67**:4062-4069 (1993); Huang et al., *Science* **264**:961-965 (1994); Macatonia et al., *Journal of Experimental Medicine* **169**:1255-1264 (1989); Bhardwaj et al., *Journal of Clinical Investigation* **94**:797-807 (1994); and Inaba et al., *Journal of Experimental Medicine* **172**:631-640 (1990).

The proteins encoded by the cDNAs may also be evaluated for their influence on the lifetime of lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Darzynkiewicz et al., *Cytometry* **13**:795-808 (1992); Gorczyca et al., *Leukemia* **7**:659-670 (1993); Gorczyca et al., *Cancer Research* **53**:1945-1951 (1993); Itoh et al., *Cell* **66**:233-243 (1991); Zacharchuk et al., *J. Immunol.* **145**:4037-4045 (1990); Zamai et al., *Cytometry* **14**:891-897 (1993); and Gorczyca et al., *International Journal of Oncology* **1**:639-648 (1992).

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., *Blood* **84**:111-117 (1994); Fine et al., *Cellular immunology* **155**:111-122 (1994); Galy et al., *Blood* **85**:2770-2778 (1995); and Toki et al., *Proc. Nat. Acad. Sci. USA* **88**:7548-7551 (1991).

Those proteins which exhibit activity as immune system regulators activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of immune activity is beneficial. For example, the protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T-

cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this manner prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., *Science* **257**:789-792 (1992) and Turka et al., *Proc. Natl. Acad. Sci USA*, **89**:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, (1989), pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms.

Administration of reagents which block costimulation of T cells by disrupting receptor ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/pr/pr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in OD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, (1989), pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory form of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to T cells in vivo, thereby activating the T cells.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acids encoding all or a portion of (e.g., a

cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 macroglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class II or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject. Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 34

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Hematopoiesis Regulating Activity

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their hematopoiesis regulating activity. For example, the effect of the proteins on embryonic stem cell differentiation may be evaluated. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Johansson et al. *Cellular Biology* **15**:141-151 (1995); Keller et al., *Molecular and Cellular Biology* **13**:473-486 (1993); and McClanahan et al., *Blood* **81**:2903-2915 (1993).

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their influence on the lifetime of stem cells and stem cell differentiation. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Freshney, M.G. Methylcellulose Colony Forming Assays, *Culture of Hematopoietic Cells*. R.I. Freshney, et al. Eds. pp. 265-268, Wiley-Liss, Inc., New York, NY. (1994); Hirayama et al., *Proc. Natl. Acad. Sci. USA* **89**:5907-5911 (1992); McNiece, I.K. and Briddell, R.A. Primitive Hematopoietic Colony Forming Cells with High Proliferative Potential, *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. (1994); Neben et al., *Experimental Hematology* **22**:353-359 (1994); Ploemacher, R.E. Cobblestone Area Forming Cell Assay, *Culture of Hematopoietic Cells*. R.I. Freshney, et al. Eds. pp. 1-21, Wiley-Liss, Inc., New York, NY. (1994); Spooncer, E., Dexter, M. and Allen, T. Long Term Bone Marrow Cultures in the Presence of Stromal Cells, *Culture of Hematopoietic Cells*. R.I. Freshney, et al. Eds. pp. 163-179, Wiley-Liss, Inc., New York, NY. (1994); and Sutherland, H.J. Long Term Culture Initiating Cell Assay, *Culture of Hematopoietic Cells*. R.I. Freshney, et al. Eds. pp. 139-162, Wiley-Liss, Inc., New York, NY. (1994).

Those proteins which exhibit hematopoiesis regulatory activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of hematopoiesis is beneficial. For example, a protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy. Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 35

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Regulation of Tissue Growth

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their effect on tissue growth. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in International Patent Publication No. WO95/16035, International Patent Publication No. WO95/05846 and International Patent Publication No. WO91/07491.

Assays for wound healing activity include, without limitation, those described in: Winter, *Epidermal Wound Healing*, pps. 71-112 (Maibach, H1 and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, *J. Invest. Dermatol.* **71**:382-84 (1978).

Those proteins which are involved in the regulation of tissue growth may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of tissue growth is beneficial. For example, a protein of the present invention also may have utility in compositions used for bone, cartilage,

tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue.

De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e., for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and

localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium) muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to generate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 36

Assaying the Proteins Expressed from Extended cDNAs or Portions

Thereof for Regulation of Reproductive Hormones or Cell Movement

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their ability to regulate reproductive hormones, such as follicle stimulating hormone. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Vale et al., *Endocrinology* **91**:562-572 (1972); Ling et al., *Nature* **321**:779-782 (1986); Vale et al., *Nature* **321**:776-779 (1986); Mason et al., *Nature* **318**:659-663 (1985); Forage et al., *Proc. Natl. Acad. Sci. USA* **83**:3091-3095 (1986). Chapter 6.12 (Measurement of Alpha and Beta Chemokines) *Current Protocols in Immunology*, J.E. Coligan et al. Eds. Greene Publishing Associates and Wiley-Interscience; Taub et al. *J. Clin. Invest.* **95**:1370-1376 (1995); Lind et al. *APMIS* **103**:140-146 (1995); Muller et al. *Eur. J. Immunol.*

25:1744-1748; Gruber et al. *J. of Immunol.* **152**:5860-5867 (1994); and Johnston et al. *J. of Immunol.* **153**:1762-1768 (1994).

Those proteins which exhibit activity as reproductive hormones or regulators of cell movement may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of reproductive hormones or cell movement are beneficial. For example, a protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-B group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 36A

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Chemotactic/Chemokinetic Activity

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for chemotactic/chemokinetic activity. For example, a protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has

chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. *J. Clin. Invest.* **95**:1370-1376 (1995); Lind et al. *APMIS* **103**:140-146 (1995); Mueller et al. *Eur. J. Immunol.* **25**:1744-1748; Gruber et al. *J. of Immunol.* **152**:5860-5867 (1994); and Johnston et al. *J. of Immunol.* **153**:1762-1768 (1994).

EXAMPLE 37

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Regulation of Blood Clotting

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their effects on blood clotting. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Linet et al., *J. Clin. Pharmacol.* **26**:131-140 (1986); Burdick et al., *Thrombosis Res.* **45**:413-419 (1987); Humphrey et al., *Fibrinolysis* **5**:71-79 (1991); and Schaub, *Prostaglandins* **35**:467-474 (1988).

Those proteins which are involved in the regulation of blood clotting may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of blood clotting is beneficial. For example, a protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulations disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke). Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 38Assaying the Proteins Expressed from Extended cDNAs or
Portions Thereof for Involvement in Receptor/Ligand Interactions

The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for their involvement in receptor/ligand interactions. Numerous assays for such involvement are familiar to those skilled in the art, including the assays disclosed in the following references: Chapter 7.28 (Measurement of Cellular Adhesion under Static Conditions 7.28.1-7.28.22) *Current Protocols in Immunology*, J.E. Coligan et al. Eds. Greene Publishing Associates and Wiley-Interscience; Takai et al., *Proc. Natl. Acad. Sci. USA* **84**:6864-6868 (1987); Bierer et al., *J. Exp. Med.* **168**:1145-1156 (1988); Rosenstein et al., *J. Exp. Med.* **169**:149-160 (1989); Stoltenborg et al., *J. Immunol. Methods* **175**:59-68 (1994); Stitt et al., *Cell* **80**:661-670 (1995); and Gyuris et al., *Cell* **75**:791-803 (1993).

For example, the proteins of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

EXAMPLE 38AAssaying the Proteins Expressed from Extended cDNAs or
Portions Thereof for Anti-Inflammatory Activity

The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the

invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

EXAMPLE 38B

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Tumor Inhibition Activity

The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for tumor inhibition activity. In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

EXAMPLE 39

Identification of Proteins which Interact with Polypeptides Encoded by Extended cDNAs

Proteins which interact with the polypeptides encoded by extended cDNAs or portions thereof, such

as receptor proteins, may be identified using two hybrid systems such as the Matchmaker Two Hybrid System 2 (Catalog No. K1604-1, Clontech). As described in the manual accompanying the Matchmaker Two Hybrid System 2 (Catalog No. K1604-1, Clontech), the extended cDNAs or portions thereof, are inserted into an expression vector such that they are in frame with DNA encoding the DNA binding domain of the yeast transcriptional activator GAL4. cDNAs in a cDNA library which encode proteins which might interact with the polypeptides encoded by the extended cDNAs or portions thereof are inserted into a second expression vector such that they are in frame with DNA encoding the activation domain of GAL4. The two expression plasmids are transformed into yeast and the yeast are plated on selection medium which selects for expression of selectable markers on each of the expression vectors as well as GAL4 dependent expression of the HIS3 gene. Transformants capable of growing on medium lacking histidine are screened for GAL4 dependent lacZ expression. Those cells which are positive in both the histidine selection and the lacZ assay contain plasmids encoding proteins which interact with the polypeptide encoded by the extended cDNAs or portions thereof.

Alternatively, the system described in Lustig et al., *Methods in Enzymology* **283**: 83-99 (1997), may be used for identifying molecules which interact with the polypeptides encoded by extended cDNAs. In such systems, *in vitro* transcription reactions are performed on a pool of vectors containing extended cDNA inserts cloned downstream of a promoter which drives *in vitro* transcription. The resulting pools of mRNAs are introduced into *Xenopus laevis* oocytes. The oocytes are then assayed for a desired activity.

Alternatively, the pooled *in vitro* transcription products produced as described above may be translated *in vitro*. The pooled *in vitro* translation products can be assayed for a desired activity or for interaction with a known polypeptide.

Proteins or other molecules interacting with polypeptides encoded by extended cDNAs can be found by a variety of additional techniques. In one method, affinity columns containing the polypeptide encoded by the extended cDNA or a portion thereof can be constructed. In some versions, of this method the affinity column contains chimeric proteins in which the protein encoded by the extended cDNA or a portion thereof is fused to glutathione S-transferase. A mixture of cellular proteins or pool of expressed proteins as described above and is applied to the affinity column. Proteins interacting with the polypeptide attached to the column can then be isolated and analyzed on 2-D electrophoresis gel as described in Ramunsen et al. *Electrophoresis* **18**:588-598 (1997). Alternatively, the proteins retained on the affinity column can be purified by electrophoresis based methods and sequenced. The same method can be used to isolate antibodies, to screen phage display products, or to screen phage display human antibodies.

Proteins interacting with polypeptides encoded by extended cDNAs or portions thereof can also be screened by using an Optical Biosensor as described in Edwards & Leatherbarrow, *Analytical Biochemistry*, **246**:1-6 (1997). The main advantage of the method is that it allows the determination of the association rate between the protein and other interacting molecules. Thus, it is possible to

specifically select interacting molecules with a high or low association rate. Typically a target molecule is linked to the sensor surface (through a carboxymethyl dextran matrix) and a sample of test molecules is placed in contact with the target molecules. The binding of a test molecule to the target molecule causes a change in the refractive index and/or thickness. This change is detected by the Biosensor provided it occurs in the evanescent field (which extend a few hundred nanometers from the sensor surface). In these screening assays, the target molecule can be one of the polypeptides encoded by extended cDNAs or a portion thereof and the test sample can be a collection of proteins extracted from tissues or cells, a pool of expressed proteins, combinatorial peptide and/ or chemical libraries, or phage displayed peptides. The tissues or cells from which the test proteins are extracted can originate from any species.

In other methods, a target protein is immobilized and the test population is a collection of unique polypeptides encoded by the extended cDNAs or portions thereof.

To study the interaction of the proteins encoded by the extended cDNAs or portions thereof with drugs, the microdialysis coupled to HPLC method described by Wang et al., *Chromatographia* **44**:205-208(1997) or the affinity capillary electrophoresis method described by Busch et al., *J. Chromatogr.* **777**:311-328 (1997).

The system described in U.S. Patent No. 5,654,150, may also be used to identify molecules which interact with the polypeptides encoded by the extended cDNAs. In this system, pools of extended cDNAs are transcribed and translated *in vitro* and the reaction products are assayed for interaction with a known polypeptide or antibody.

It will be appreciated by those skilled in the art that the proteins expressed from the extended cDNAs or portions may be assayed for numerous activities in addition to those specifically enumerated above. For example, the expressed proteins may be evaluated for applications involving control and regulation of inflammation, tumor proliferation or metastasis, infection, or other clinical conditions. In addition, the proteins expressed from the extended cDNAs or portions thereof may be useful as nutritional agents or cosmetic agents.

The proteins expressed from the extended cDNAs or portions thereof may be used to generate antibodies capable of specifically binding to the expressed protein or fragments thereof as described in Example 40 below. The antibodies may be capable of binding a full length protein encoded by one of the sequences of SEQ ID NOs. 134-180, a mature protein encoded by one of the sequences of SEQ ID NOs. 134-180, or a signal peptide encoded by one of the sequences of SEQ ID Nos. 134-180. Alternatively, the antibodies may be capable of binding fragments of the proteins expressed from the extended cDNAs which comprise at least 10 amino acids of the sequences of SEQ ID NOs: 181-227. In some embodiments, the antibodies may be capable of binding fragments of the proteins expressed from the extended cDNAs which comprise at least 15 amino acids of the sequences of SEQ ID NOs: 181-227. In other embodiments, the antibodies may be capable of binding fragments of the proteins expressed from the extended cDNAs which comprise at least 25 amino acids of the sequences of SEQ ID NOs: 181-227. In further embodiments, the

antibodies may be capable of binding fragments of the proteins expressed from the extended cDNAs which comprise at least 40 amino acids of the sequences of SEQ ID NOs: 181-227.

EXAMPLE 40

Production of an Antibody to a Human Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells as described in Example 30. The concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows:

A. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature* **256**:495 (1975) or derivative methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as Elisa, as originally described by Engvall, E., *Meth. Enzymol.* **70**:419 (1980), and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. et al. *Basic Methods in Molecular Biology* Elsevier, New York. Section 21-2.

B. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein or peptides derived therefrom described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. et al. *J. Clin. Endocrinol. Metab.* **33**:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. et al., Chap. 19 in:

Handbook of Experimental Immunology D. Wier (ed) Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μ M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, 2d Ed. (Rose and Friedman, Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980).

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies may also be used in therapeutic compositions for killing cells expressing the protein or reducing the levels of the protein in the body.

V. Use of Extended cDNAs or Portions Thereof as Reagents

The extended cDNAs of the present invention may be used as reagents in isolation procedures, diagnostic assays, and forensic procedures. For example, sequences from the extended cDNAs (or genomic DNAs obtainable therefrom) may be detectably labeled and used as probes to isolate other sequences capable of hybridizing to them. In addition, sequences from the extended cDNAs (or genomic DNAs obtainable therefrom) may be used to design PCR primers to be used in isolation, diagnostic, or forensic procedures.

EXAMPLE 41

Preparation of PCR Primers and Amplification of DNA

The extended cDNAs (or genomic DNAs obtainable therefrom) may be used to prepare PCR primers for a variety of applications, including isolation procedures for cloning nucleic acids capable of hybridizing to such sequences, diagnostic techniques and forensic techniques. The PCR primers are at least 10 bases, and preferably at least 12, 15, or 17 bases in length. More preferably, the PCR primers are at least 20-30 bases in length. In some embodiments, the PCR primers may be more than 30 bases in length. It is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering White, B.A. Ed. in *Methods in Molecular Biology* 67: Humana Press, Totowa (1997). In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

EXAMPLE 42Use of Extended cDNAs as Probes

Probes derived from extended cDNAs or portions thereof (or genomic DNAs obtainable therefrom) may be labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-radioactive labels, to provide a detectable probe. The detectable probe may be single stranded or double stranded and may be made using techniques known in the art, including in vitro transcription, nick translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the nucleic acid in the sample is double stranded, it may be denatured prior to contacting the probe. In some applications, the nucleic acid sample may be immobilized on a surface such as a nitrocellulose or nylon membrane. The nucleic acid sample may comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony hybridization, and plaque hybridization. In some applications, the nucleic acid capable of hybridizing to the labeled probe may be cloned into vectors such as expression vectors, sequencing vectors, or in vitro transcription vectors to facilitate the characterization and expression of the hybridizing nucleic acids in the sample. For example, such techniques may be used to isolate and clone sequences in a genomic library or cDNA library which are capable of hybridizing to the detectable probe as described in Example 30 above.

PCR primers made as described in Example 41 above may be used in forensic analyses, such as the DNA fingerprinting techniques described in Examples 43-47 below. Such analyses may utilize detectable probes or primers based on the sequences of the extended cDNAs isolated using the 5' ESTs (or genomic DNAs obtainable therefrom).

EXAMPLE 43Forensic Matching by DNA Sequencing

In one exemplary method, DNA samples are isolated from forensic specimens of, for example, hair, semen, blood or skin cells by conventional methods. A panel of PCR primers based on a number of the extended cDNAs (or genomic DNAs obtainable therefrom), is then utilized in accordance with Example 41 to amplify DNA of approximately 100-200 bases in length from the forensic specimen. Corresponding sequences are obtained from a test subject. Each of these identification DNAs is then sequenced using standard techniques, and a simple database comparison determines the differences, if any, between the sequences from the subject and those from the sample. Statistically significant differences between the suspect's DNA sequences and those from the sample conclusively prove a lack of identity. This lack of identity can be proven, for example, with only one sequence. Identity, on the other hand, should be demonstrated with a large number of sequences, all matching. Preferably, a minimum of 50 statistically

identical sequences of 100 bases in length are used to prove identity between the suspect and the sample.

EXAMPLE 44

Positive Identification by DNA Sequencing

The technique outlined in the previous example may also be used on a larger scale to provide a unique fingerprint-type identification of any individual. In this technique, primers are prepared from a large number of sequences from Table II and the appended sequence listing. Preferably, 20 to 50 different primers are used. These primers are used to obtain a corresponding number of PCR-generated DNA segments from the individual in question in accordance with Example 41. Each of these DNA segments is sequenced, using the methods set forth in Example 43. The database of sequences generated through this procedure uniquely identifies the individual from whom the sequences were obtained. The same panel of primers may then be used at any later time to absolutely correlate tissue or other biological specimen with that individual.

EXAMPLE 45

Southern Blot Forensic Identification

The procedure of Example 44 is repeated to obtain a panel of at least 10 amplified sequences from an individual and a specimen. Preferably, the panel contains at least 50 amplified sequences. More preferably, the panel contains 100 amplified sequences. In some embodiments, the panel contains 200 amplified sequences. This PCR-generated DNA is then digested with one or a combination of, preferably, four base specific restriction enzymes. Such enzymes are commercially available and known to those of skill in the art. After digestion, the resultant gene fragments are size separated in multiple duplicate wells on an agarose gel and transferred to nitrocellulose using Southern blotting techniques well known to those with skill in the art. For a review of Southern blotting see Davis et al. *Basic Methods in Molecular Biology*, (1986), Elsevier Press. pp 62-65).

A panel of probes based on the sequences of the extended cDNAs (or genomic DNAs obtainable therefrom), or fragments thereof of at least 10 bases, are radioactively or colorimetrically labeled using methods known in the art, such as nick translation or end labeling, and hybridized to the Southern blot using techniques known in the art (Davis et al., *supra*). Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the extended cDNA (or genomic DNAs obtainable therefrom). More preferably, the probe comprises at least 20-30 consecutive nucleotides from the extended cDNA (or genomic DNAs obtainable therefrom). In some embodiments, the probe comprises more than 30 nucleotides from the extended cDNA (or genomic DNAs obtainable therefrom).

Preferably, at least 5 to 10 of these labeled probes are used, and more preferably at least about 20 or 30 are used to provide a unique pattern. The resultant bands appearing from the hybridization of a large sample of extended cDNAs (or genomic DNAs obtainable therefrom) will be a unique identifier. Since the

restriction enzyme cleavage will be different for every individual, the band pattern on the Southern blot will also be unique. Increasing the number of extended cDNA probes will provide a statistically higher level of confidence in the identification since there will be an increased number of sets of bands used for identification.

EXAMPLE 46

Dot Blot Identification Procedure

Another technique for identifying individuals using the extended cDNA sequences disclosed herein utilizes a dot blot hybridization technique.

Genomic DNA is isolated from nuclei of subject to be identified. Oligonucleotide probes of approximately 30 bp in length are synthesized that correspond to at least 10, preferably 50 sequences from the extended cDNAs or genomic DNAs obtainable therefrom. The probes are used to hybridize to the genomic DNA through conditions known to those in the art. The oligonucleotides are end labeled with P^{32} using polynucleotide kinase (Pharmacia). Dot Blots are created by spotting the genomic DNA onto nitrocellulose or the like using a vacuum dot blot manifold (BioRad, Richmond California). The nitrocellulose filter containing the genomic sequences is baked or UV linked to the filter, prehybridized and hybridized with labeled probe using techniques known in the art (Davis et al. *supra*). The ^{32}P labeled DNA fragments are sequentially hybridized with successively stringent conditions to detect minimal differences between the 30 bp sequence and the DNA. Tetramethylammonium chloride is useful for identifying clones containing small numbers of nucleotide mismatches (Wood et al., *Proc. Natl. Acad. Sci. USA* **82(6)**:1585-1588 (1985)). A unique pattern of dots distinguishes one individual from another individual.

Extended cDNAs or oligonucleotides containing at least 10 consecutive bases from these sequences can be used as probes in the following alternative fingerprinting technique. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the extended cDNA (or genomic DNAs obtainable therefrom). More preferably, the probe comprises at least 20-30 consecutive nucleotides from the extended cDNA (or genomic DNAs obtainable therefrom). In some embodiments, the probe comprises more than 30 nucleotides from the extended cDNA (or genomic DNAs obtainable therefrom).

Preferably, a plurality of probes having sequences from different genes are used in the alternative fingerprinting technique. Example 47 below provides a representative alternative fingerprinting procedure in which the probes are derived from extended cDNAs.

EXAMPLE 47

Alternative "Fingerprint" Identification Technique

20-mer oligonucleotides are prepared from a large number, e.g. 50, 100, or 200, of extended cDNA sequences (or genomic DNAs obtainable therefrom) using commercially available oligonucleotide services such as Genset, Paris, France. Cell samples from the test subject are processed for DNA using

techniques well known to those with skill in the art. The nucleic acid is digested with restriction enzymes such as EcoRI and XbaI. Following digestion, samples are applied to wells for electrophoresis. The procedure, as known in the art, may be modified to accommodate polyacrylamide electrophoresis, however in this example, samples containing 5 ug of DNA are loaded into wells and separated on 0.8% agarose gels.

The gels are transferred onto nitrocellulose using standard Southern blotting techniques.

10 ng of each of the oligonucleotides are pooled and end-labeled with P^{32} . The nitrocellulose is prehybridized with blocking solution and hybridized with the labeled probes. Following hybridization and washing, the nitrocellulose filter is exposed to X-Omat AR X-ray film. The resulting hybridization pattern will be unique for each individual.

It is additionally contemplated within this example that the number of probe sequences used can be varied for additional accuracy or clarity.

The antibodies generated in Examples 30 and 40 above may be used to identify the tissue type or cell species from which a sample is derived as described above.

EXAMPLE 48

Identification of Tissue Types or Cell Species by Means of Labeled Tissue Specific Antibodies

Identification of specific tissues is accomplished by the visualization of tissue specific antigens by means of antibody preparations according to Examples 30 and 40 which are conjugated, directly or indirectly to a detectable marker. Selected labeled antibody species bind to their specific antigen binding partner in tissue sections, cell suspensions, or in extracts of soluble proteins from a tissue sample to provide a pattern for qualitative or semi-qualitative interpretation.

Antisera for these procedures must have a potency exceeding that of the native preparation, and for that reason, antibodies are concentrated to a mg/ml level by isolation of the gamma globulin fraction, for example, by ion-exchange chromatography or by ammonium sulfate fractionation. Also, to provide the most specific antisera, unwanted antibodies, for example to common proteins, must be removed from the gamma globulin fraction, for example by means of insoluble immunoabsorbents, before the antibodies are labeled with the marker. Either monoclonal or heterologous antisera is suitable for either procedure.

A. Immunohistochemical Techniques

Purified, high-titer antibodies, prepared as described above, are conjugated to a detectable marker, as described, for example, by Fudenberg, H., Chap. 26 in: *Basic 503 Clinical Immunology*, 3rd Ed. Lange, Los Altos, California (1980) or Rose, N. et al., Chap. 12 in: *Methods in Immunodiagnosis*, 2d Ed. John Wiley 503 Sons, New York (1980).

A fluorescent marker, either fluorescein or rhodamine, is preferred, but antibodies can also be labeled with an enzyme that supports a color producing reaction with a substrate, such as horseradish peroxidase. Markers can be added to tissue-bound antibody in a second step, as described below.

Alternatively, the specific antitissue antibodies can be labeled with ferritin or other electron dense particles, and localization of the ferritin coupled antigen-antibody complexes achieved by means of an electron microscope. In yet another approach, the antibodies are radiolabeled, with, for example ^{125}I , and detected by overlaying the antibody treated preparation with photographic emulsion.

Preparations to carry out the procedures can comprise monoclonal or polyclonal antibodies to a single protein or peptide identified as specific to a tissue type, for example, brain tissue, or antibody preparations to several antigenically distinct tissue specific antigens can be used in panels, independently or in mixtures, as required.

Tissue sections and cell suspensions are prepared for immunohistochemical examination according to common histological techniques. Multiple cryostat sections (about 4 μm , unfixed) of the unknown tissue and known control, are mounted and each slide covered with different dilutions of the antibody preparation. Sections of known and unknown tissues should also be treated with preparations to provide a positive control, a negative control, for example, pre-immune sera, and a control for non-specific staining, for example, buffer.

Treated sections are incubated in a humid chamber for 30 min at room temperature, rinsed, then washed in buffer for 30-45 min. Excess fluid is blotted away, and the marker developed.

If the tissue specific antibody was not labeled in the first incubation, it can be labeled at this time in a second antibody-antibody reaction, for example, by adding fluorescein- or enzyme-conjugated antibody against the immunoglobulin class of the antiserum-producing species, for example, fluorescein labeled antibody to mouse IgG. Such labeled sera are commercially available.

The antigen found in the tissues by the above procedure can be quantified by measuring the intensity of color or fluorescence on the tissue section, and calibrating that signal using appropriate standards.

B. Identification of Tissue Specific Soluble Proteins

The visualization of tissue specific proteins and identification of unknown tissues from that procedure is carried out using the labeled antibody reagents and detection strategy as described for immunohistochemistry; however the sample is prepared according to an electrophoretic technique to distribute the proteins extracted from the tissue in an orderly array on the basis of molecular weight for detection.

A tissue sample is homogenized using a Virtis apparatus; cell suspensions are disrupted by Dounce homogenization or osmotic lysis, using detergents in either case as required to disrupt cell membranes, as is the practice in the art. Insoluble cell components such as nuclei, microsomes, and membrane fragments are removed by ultracentrifugation, and the soluble protein-containing fraction concentrated if necessary and reserved for analysis.

A sample of the soluble protein solution is resolved into individual protein species by conventional SDS polyacrylamide electrophoresis as described, for example, by Davis, L. et al., Section 19-2 in: *Basic*

Methods in Molecular Biology (P. Leder, ed), Elsevier, New York (1986), using a range of amounts of polyacrylamide in a set of gels to resolve the entire molecular weight range of proteins to be detected in the sample. A size marker is run in parallel for purposes of estimating molecular weights of the constituent proteins. Sample size for analysis is a convenient volume of from 5 to 55 μ l, and containing from about 1 to 100 μ g protein. An aliquot of each of the resolved proteins is transferred by blotting to a nitrocellulose filter paper, a process that maintains the pattern of resolution. Multiple copies are prepared. The procedure, known as Western Blot Analysis, is well described in Davis, L. et al., (above) Section 19-3. One set of nitrocellulose blots is stained with Coomassie Blue dye to visualize the entire set of proteins for comparison with the antibody bound proteins. The remaining nitrocellulose filters are then incubated with a solution of one or more specific antisera to tissue specific proteins prepared as described in Examples 30 and 40. In this procedure, as in procedure A above, appropriate positive and negative sample and reagent controls are run.

In either procedure A or B, a detectable label can be attached to the primary tissue antigen-primary antibody complex according to various strategies and permutations thereof. In a straightforward approach, the primary specific antibody can be labeled; alternatively, the unlabeled complex can be bound by a labeled secondary anti-IgG antibody. In other approaches, either the primary or secondary antibody is conjugated to a biotin molecule, which can, in a subsequent step, bind an avidin conjugated marker. According to yet another strategy, enzyme labeled or radioactive protein A, which has the property of binding to any IgG, is bound in a final step to either the primary or secondary antibody.

The visualization of tissue specific antigen binding at levels above those seen in control tissues to one or more tissue specific antibodies, prepared from the gene sequences identified from extended cDNA sequences, can identify tissues of unknown origin, for example, forensic samples, or differentiated tumor tissue that has metastasized to foreign bodily sites.

In addition to their applications in forensics and identification, extended cDNAs (or genomic DNAs obtainable therefrom) may be mapped to their chromosomal locations. Example 49 below describes radiation hybrid (RH) mapping of human chromosomal regions using extended cDNAs. Example 50 below describes a representative procedure for mapping an extended cDNA (or a genomic DNA obtainable therefrom) to its location on a human chromosome. Example 51 below describes mapping of extended cDNAs (or genomic DNAs obtainable therefrom) on metaphase chromosomes by Fluorescence In Situ Hybridization (FISH).

EXAMPLE 49

Radiation hybrid mapping of Extended cDNAs to the human genome

Radiation hybrid (RH) mapping is a somatic cell genetic approach that can be used for high resolution mapping of the human genome. In this approach, cell lines containing one or more human chromosomes are lethally irradiated, breaking each chromosome into fragments whose size depends on the radiation dose. These fragments are rescued by fusion with cultured rodent cells, yielding subclones

containing different portions of the human genome. This technique is described by Benham et al. *Genomics* 4:509-517 (1989) and Cox et al., *Science* 250:245-250 (1990). The random and independent nature of the subclones permits efficient mapping of any human genome marker. Human DNA isolated from a panel of 80-100 cell lines provides a mapping reagent for ordering extended cDNAs (or genomic DNAs obtainable therefrom). In this approach, the frequency of breakage between markers is used to measure distance, allowing construction of fine resolution maps as has been done using conventional ESTs Schuler et al., *Science* 274:540-546 (1996).

RH mapping has been used to generate a high-resolution whole genome radiation hybrid map of human chromosome 17q22-q25.3 across the genes for growth hormone (GH) and thymidine kinase (TK) Foster et al., *Genomics* 33:185-192 (1996), the region surrounding the Gorlin syndrome gene (Obermayr et al., *Eur. J. Hum. Genet.* 4:242-245, 1996), 60 loci covering the entire short arm of chromosome 12 (Raeymaekers et al., *Genomics* 29:170-178, (1995)), the region of human chromosome 22 containing the neurofibromatosis type 2 locus (Frazer et al., *Genomics* 14:574-584 (1992)) and 13 loci on the long arm of chromosome 5 (Warrington et al., *Genomics* 11:701-708 (1991)).

EXAMPLE 50

Mapping of Extended cDNAs to Human Chromosomes using PCR techniques

Extended cDNAs (or genomic DNAs obtainable therefrom) may be assigned to human chromosomes using PCR based methodologies. In such approaches, oligonucleotide primer pairs are designed from the extended cDNA sequence (or the sequence of a genomic DNA obtainable therefrom) to minimize the chance of amplifying through an intron. Preferably, the oligonucleotide primers are 18-23 bp in length and are designed for PCR amplification. The creation of PCR primers from known sequences is well known to those with skill in the art. For a review of PCR technology see Erlich, H.A., *PCR Technology; Principles and Applications for DNA Amplification*. (1992). W.H. Freeman and Co., New York.

The primers are used in polymerase chain reactions (PCR) to amplify templates from total human genomic DNA. PCR conditions are as follows: 60 ng of genomic DNA is used as a template for PCR with 80 ng of each oligonucleotide primer, 0.6 unit of Taq polymerase, and 1 μ Cu of a 32 P-labeled deoxycytidine triphosphate. The PCR is performed in a microplate thermocycler (Techne) under the following conditions: 30 cycles of 94°C, 1.4 min; 55°C, 2 min; and 72°C, 2 min; with a final extension at 72°C for 10 min. The amplified products are analyzed on a 6% polyacrylamide sequencing gel and visualized by autoradiography. If the length of the resulting PCR product is identical to the distance between the ends of the primer sequences in the extended cDNA from which the primers are derived, then the PCR reaction is repeated with DNA templates from two panels of human-rodent somatic cell hybrids, BIOS PCRable DNA (BIOS Corporation) and NIGMS Human-Rodent Somatic Cell Hybrid Mapping Panel Number 1 (NIGMS,

Camden, NJ).

PCR is used to screen a series of somatic cell hybrid cell lines containing defined sets of human chromosomes for the presence of a given extended cDNA (or genomic DNA obtainable therefrom). DNA is isolated from the somatic hybrids and used as starting templates for PCR reactions using the primer pairs from the extended cDNAs (or genomic DNAs obtainable therefrom). Only those somatic cell hybrids with chromosomes containing the human gene corresponding to the extended cDNA (or genomic DNA obtainable therefrom) will yield an amplified fragment. The extended cDNAs (or genomic DNAs obtainable therefrom) are assigned to a chromosome by analysis of the segregation pattern of PCR products from the somatic hybrid DNA templates. The single human chromosome present in all cell hybrids that give rise to an amplified fragment is the chromosome containing that extended cDNA (or genomic DNA obtainable therefrom). For a review of techniques and analysis of results from somatic cell gene mapping experiments. (See Ledbetter et al., *Genomics* 6:475-481 (1990).)

Alternatively, the extended cDNAs (or genomic DNAs obtainable therefrom) may be mapped to individual chromosomes using FISH as described in Example 51 below.

EXAMPLE 51

Mapping of Extended 5' ESTs to Chromosomes

Using Fluorescence in situ Hybridization

Fluorescence in situ hybridization allows the extended cDNA (or genomic DNA obtainable therefrom) to be mapped to a particular location on a given chromosome. The chromosomes to be used for fluorescence in situ hybridization techniques may be obtained from a variety of sources including cell cultures, tissues, or whole blood.

In a preferred embodiment, chromosomal localization of an extended cDNA (or genomic DNA obtainable therefrom) is obtained by FISH as described by Cherif et al. *Proc. Natl. Acad. Sci. U.S.A.*, 87:6639-6643 (1990). Metaphase chromosomes are prepared from phytohemagglutinin (PHA)-stimulated blood cell donors. PHA-stimulated lymphocytes from healthy males are cultured for 72 h in RPMI-1640 medium. For synchronization, methotrexate (10 μ M) is added for 17 h, followed by addition of 5-bromodeoxyuridine (5-BudR, 0.1 mM) for 6 h. Colcemid (1 μ g/ml) is added for the last 15 min before harvesting the cells. Cells are collected, washed in RPMI, incubated with a hypotonic solution of KCl (75 mM) at 37°C for 15 min and fixed in three changes of methanol:acetic acid (3:1). The cell suspension is dropped onto a glass slide and air dried. The extended cDNA (or genomic DNA obtainable therefrom) is labeled with biotin-16 dUTP by nick translation according to the manufacturer's instructions (Bethesda Research Laboratories, Bethesda, MD), purified using a Sephadex G-50 column (Pharmacia, Upssala, Sweden) and precipitated. Just prior to hybridization, the DNA pellet is dissolved in hybridization buffer (50% formamide, 2 X SSC, 10% dextran sulfate, 1 mg/ml sonicated salmon sperm DNA, pH 7) and the probe is denatured at 70°C for 5-10 min.

Slides kept at -20°C are treated for 1 h at 37°C with RNase A (100 µg/ml), rinsed three times in 2 X SSC and dehydrated in an ethanol series. Chromosome preparations are denatured in 70% formamide, 2 X SSC for 2 min at 70°C, then dehydrated at 4°C. The slides are treated with proteinase K (10 µg/100 ml in 20 mM Tris-HCl, 2 mM CaCl₂) at 37°C for 8 min and dehydrated. The hybridization mixture containing the probe is placed on the slide, covered with a coverslip, sealed with rubber cement and incubated overnight in a humid chamber at 37°C. After hybridization and post-hybridization washes, the biotinylated probe is detected by avidin-FITC and amplified with additional layers of biotinylated goat anti-avidin and avidin-FITC. For chromosomal localization, fluorescent R-bands are obtained as previously described (Cherif et al., *supra.*). The slides are observed under a LEICA fluorescence microscope (DMRXA). Chromosomes are counterstained with propidium iodide and the fluorescent signal of the probe appears as two symmetrical yellow-green spots on both chromatids of the fluorescent R-band chromosome (red). Thus, a particular extended cDNA (or genomic DNA obtainable therefrom) may be localized to a particular cytogenetic R-band on a given chromosome.

Once the extended cDNAs (or genomic DNAs obtainable therefrom) have been assigned to particular chromosomes using the techniques described in Examples 49-51 above, they may be utilized to construct a high resolution map of the chromosomes on which they are located or to identify the chromosomes in a sample.

EXAMPLE 52

Use of Extended cDNAs to Construct or Expand Chromosome Maps

Chromosome mapping involves assigning a given unique sequence to a particular chromosome as described above. Once the unique sequence has been mapped to a given chromosome, it is ordered relative to other unique sequences located on the same chromosome. One approach to chromosome mapping utilizes a series of yeast artificial chromosomes (YACs) bearing several thousand long inserts derived from the chromosomes of the organism from which the extended cDNAs (or genomic DNAs obtainable therefrom) are obtained. This approach is described in Ramaiah Nagaraja et al. *Genome Research* 7:210-222, (March, 1997). Briefly, in this approach each chromosome is broken into overlapping pieces which are inserted into the YAC vector. The YAC inserts are screened using PCR or other methods to determine whether they include the extended cDNA (or genomic DNA obtainable therefrom) whose position is to be determined. Once an insert has been found which includes the extended cDNA (or genomic DNA obtainable therefrom), the insert can be analyzed by PCR or other methods to determine whether the insert also contains other sequences known to be on the chromosome or in the region from which the extended cDNA (or genomic DNA obtainable therefrom) was derived. This process can be repeated for each insert in the YAC library to determine the location of each of the extended cDNAs (or genomic DNAs obtainable therefrom) relative to one another and to other known chromosomal markers. In this way, a high resolution map of the distribution of numerous unique markers along each of the organisms chromosomes may be

obtained.

As described in Example 53 below extended cDNAs (or genomic DNAs obtainable therefrom) may also be used to identify genes associated with a particular phenotype, such as hereditary disease or drug response.

5

EXAMPLE 53

Identification of genes associated with hereditary diseases or drug response

This example illustrates an approach useful for the association of extended cDNAs (or genomic DNAs obtainable therefrom) with particular phenotypic characteristics. In this example, a particular
10 extended cDNA (or genomic DNA obtainable therefrom) is used as a test probe to associate that extended cDNA (or genomic DNA obtainable therefrom) with a particular phenotypic characteristic.

Extended cDNAs (or genomic DNAs obtainable therefrom) are mapped to a particular location on a human chromosome using techniques such as those described in Examples 49 and 50 or other techniques known in the art. A search of Mendelian Inheritance in Man (V. McKusick, *Mendelian Inheritance in Man*
15 (available on line through Johns Hopkins University Welch Medical Library) reveals the region of the human chromosome which contains the extended cDNA (or genomic DNA obtainable therefrom) to be a very gene rich region containing several known genes and several diseases or phenotypes for which genes have not been identified. The gene corresponding to this extended cDNA (or genomic DNA obtainable therefrom) thus becomes an immediate candidate for each of these genetic diseases.

Cells from patients with these diseases or phenotypes are isolated and expanded in culture. PCR primers from the extended cDNA (or genomic DNA obtainable therefrom) are used to screen genomic DNA, mRNA or cDNA obtained from the patients. Extended cDNAs (or genomic DNAs obtainable therefrom) that are not amplified in the patients can be positively associated with a particular disease by further analysis. Alternatively, the PCR analysis may yield fragments of different lengths when the samples
20 are derived from an individual having the phenotype associated with the disease than when the sample is derived from a healthy individual, indicating that the gene containing the extended cDNA may be responsible for the genetic disease.

VI. Use of Extended cDNAs (or genomic DNAs obtainable therefrom) to Construct Vectors

The present extended cDNAs (or genomic DNAs obtainable therefrom) may also be used to
30 construct secretion vectors capable of directing the secretion of the proteins encoded by genes inserted in the vectors. Such secretion vectors may facilitate the purification or enrichment of the proteins encoded by genes inserted therein by reducing the number of background proteins from which the desired protein must be purified or enriched. Exemplary secretion vectors are described in Example 54 below.

35

EXAMPLE 54Construction of Secretion Vectors

The secretion vectors of the present invention include a promoter capable of directing gene expression in the host cell, tissue, or organism of interest. Such promoters include the Rous Sarcoma Virus promoter, the SV40 promoter, the human cytomegalovirus promoter, and other promoters familiar to those skilled in the art.

A signal sequence from an extended cDNA (or genomic DNA obtainable therefrom), such as one of the signal sequences in SEQ ID NOs: 134-180 as defined in Table VII above, is operably linked to the promoter such that the mRNA transcribed from the promoter will direct the translation of the signal peptide.

The host cell, tissue, or organism may be any cell, tissue, or organism which recognizes the signal peptide encoded by the signal sequence in the extended cDNA (or genomic DNA obtainable therefrom). Suitable hosts include mammalian cells, tissues or organisms, avian cells, tissues, or organisms, insect cells, tissues or organisms, or yeast.

In addition, the secretion vector contains cloning sites for inserting genes encoding the proteins which are to be secreted. The cloning sites facilitate the cloning of the insert gene in frame with the signal sequence such that a fusion protein in which the signal peptide is fused to the protein encoded by the inserted gene is expressed from the mRNA transcribed from the promoter. The signal peptide directs the extracellular secretion of the fusion protein.

The secretion vector may be DNA or RNA and may integrate into the chromosome of the host, be stably maintained as an extrachromosomal replicon in the host, be an artificial chromosome, or be transiently present in the host. Many nucleic acid backbones suitable for use as secretion vectors are known to those skilled in the art, including retroviral vectors, SV40 vectors, Bovine Papilloma Virus vectors, yeast integrating plasmids, yeast episomal plasmids, yeast artificial chromosomes, human artificial chromosomes, P element vectors, baculovirus vectors, or bacterial plasmids capable of being transiently introduced into the host.

The secretion vector may also contain a polyA signal such that the polyA signal is located downstream of the gene inserted into the secretion vector.

After the gene encoding the protein for which secretion is desired is inserted into the secretion vector, the secretion vector is introduced into the host cell, tissue, or organism using calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection, viral particles or as naked DNA. The protein encoded by the inserted gene is then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, immunoprecipitation, immunochromatography, size exclusion chromatography, ion exchange chromatography, and hplc. Alternatively, the secreted protein may be in a sufficiently enriched or pure state in the supernatant or growth media of the host to permit it to be used for its intended purpose without further enrichment.

The signal sequences may also be inserted into vectors designed for gene therapy. In such vectors,

the signal sequence is operably linked to a promoter such that mRNA transcribed from the promoter encodes the signal peptide. A cloning site is located downstream of the signal sequence such that a gene encoding a protein whose secretion is desired may readily be inserted into the vector and fused to the signal sequence. The vector is introduced into an appropriate host cell. The protein expressed from the promoter is secreted extracellularly, thereby producing a therapeutic effect.

The extended cDNAs or 5' ESTs may also be used to clone sequences located upstream of the extended cDNAs or 5' ESTs which are capable of regulating gene expression, including promoter sequences, enhancer sequences, and other upstream sequences which influence transcription or translation levels. Once identified and cloned, these upstream regulatory sequences may be used in expression vectors designed to direct the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative fashion. Example 55 describes a method for cloning sequences upstream of the extended cDNAs or 5' ESTs.

EXAMPLE 55

Use of Extended cDNAs or 5' ESTs to Clone Upstream Sequences from Genomic DNA

Sequences derived from extended cDNAs or 5' ESTs may be used to isolate the promoters of the corresponding genes using chromosome walking techniques. In one chromosome walking technique, which utilizes the GenomeWalker™ kit available from Clontech, five complete genomic DNA samples are each digested with a different restriction enzyme which has a 6 base recognition site and leaves a blunt end. Following digestion, oligonucleotide adapters are ligated to each end of the resulting genomic DNA fragments.

For each of the five genomic DNA libraries, a first PCR reaction is performed according to the manufacturer's instructions using an outer adaptor primer provided in the kit and an outer gene specific primer. The gene specific primer should be selected to be specific for the extended cDNA or 5' EST of interest and should have a melting temperature, length, and location in the extended cDNA or 5' EST which is consistent with its use in PCR reactions. Each first PCR reaction contains 5ng of genomic DNA, 5 µl of 10X Tth reaction buffer, 0.2 mM of each dNTP, 0.2 µM each of outer adaptor primer and outer gene specific primer, 1.1 mM of Mg(OAc)₂, and 1 µl of the Tth polymerase 50X mix in a total volume of 50 µl. The reaction cycle for the first PCR reaction is as follows: 1 min - 94°C / 2 sec - 94°C, 3 min - 72°C (7 cycles) / 2 sec - 94°C, 3 min - 67°C (32 cycles) / 5 min - 67°C.

The product of the first PCR reaction is diluted and used as a template for a second PCR reaction according to the manufacturer's instructions using a pair of nested primers which are located internally on the amplicon resulting from the first PCR reaction. For example, 5 µl of the reaction product of the first PCR reaction mixture may be diluted 180 times. Reactions are made in a 50 µl volume having a composition identical to that of the first PCR reaction except the nested primers are used. The first nested

primer is specific for the adaptor, and is provided with the GenomeWalker™ kit. The second nested primer is specific for the particular extended cDNA or 5' EST for which the promoter is to be cloned and should have a melting temperature, length, and location in the extended cDNA or 5' EST which is consistent with its use in PCR reactions. The reaction parameters of the second PCR reaction are as follows: 1 min - 94°C / 2 sec - 94°C, 3 min - 72°C (6 cycles) / 2 sec - 94°C, 3 min - 67°C (25 cycles) / 5 min - 67°C

The product of the second PCR reaction is purified, cloned, and sequenced using standard techniques. Alternatively, two or more human genomic DNA libraries can be constructed by using two or more restriction enzymes. The digested genomic DNA is cloned into vectors which can be converted into single stranded, circular, or linear DNA. A biotinylated oligonucleotide comprising at least 15 nucleotides from the extended cDNA or 5' EST sequence is hybridized to the single stranded DNA. Hybrids between the biotinylated oligonucleotide and the single stranded DNA containing the extended cDNA or EST sequence are isolated as described in Example 29 above. Thereafter, the single stranded DNA containing the extended cDNA or EST sequence is released from the beads and converted into double stranded DNA using a primer specific for the extended cDNA or 5' EST sequence or a primer corresponding to a sequence included in the cloning vector. The resulting double stranded DNA is transformed into bacteria. DNAs containing the 5' EST or extended cDNA sequences are identified by colony PCR or colony hybridization.

Once the upstream genomic sequences have been cloned and sequenced as described above, prospective promoters and transcription start sites within the upstream sequences may be identified by comparing the sequences upstream of the extended cDNAs or 5' ESTs with databases containing known transcription start sites, transcription factor binding sites, or promoter sequences.

In addition, promoters in the upstream sequences may be identified using promoter reporter vectors as described in Example 56.

EXAMPLE 56

Identification of Promoters in Cloned Upstream Sequences

The genomic sequences upstream of the extended cDNAs or 5' ESTs are cloned into a suitable promoter reporter vector, such as the pSEAP-Basic, pSEAP-Enhancer, pβgal-Basic, pβgal-Enhancer, or pEGFP-1 Promoter Reporter vectors available from Clontech. Briefly, each of these promoter reporter vectors include multiple cloning sites positioned upstream of a reporter gene encoding a readily assayable protein such as secreted alkaline phosphatase, β galactosidase, or green fluorescent protein. The sequences upstream of the extended cDNAs or 5' ESTs are inserted into the cloning sites upstream of the reporter gene in both orientations and introduced into an appropriate host cell. The level of reporter protein is assayed and compared to the level obtained from a vector which lacks an insert in the cloning site. The presence of an elevated expression level in the vector containing the insert with respect to the control vector indicates the presence of a promoter in the insert. If necessary, the upstream sequences can be cloned into vectors which contain an enhancer for augmenting transcription levels from weak promoter sequences. A

significant level of expression above that observed with the vector lacking an insert indicates that a promoter sequence is present in the inserted upstream sequence.

Appropriate host cells for the promoter reporter vectors may be chosen based on the results of the above described determination of expression patterns of the extended cDNAs and ESTs. For example, if the expression pattern analysis indicates that the mRNA corresponding to a particular extended cDNA or 5' EST is expressed in fibroblasts, the promoter reporter vector may be introduced into a human fibroblast cell line.

Promoter sequences within the upstream genomic DNA may be further defined by constructing nested deletions in the upstream DNA using conventional techniques such as Exonuclease III digestion. The resulting deletion fragments can be inserted into the promoter reporter vector to determine whether the deletion has reduced or obliterated promoter activity. In this way, the boundaries of the promoters may be defined. If desired, potential individual regulatory sites within the promoter may be identified using site directed mutagenesis or linker scanning to obliterate potential transcription factor binding sites within the promoter individually or in combination. The effects of these mutations on transcription levels may be determined by inserting the mutations into the cloning sites in the promoter reporter vectors.

EXAMPLE 57

Cloning and Identification of Promoters

Using the method described in Example 55 above with 5' ESTs, sequences upstream of several genes were obtained. Using the primer pairs GGG AAG ATG GAG ATA GTA TTG CCT G (SEQ ID NO:29) and CTG CCA TGT ACA TGA TAG AGA GAT TC (SEQ ID NO:30), the promoter having the internal designation P13H2 (SEQ ID NO:31) was obtained.

Using the primer pairs GTA CCA GGGG ACT GTG ACC ATT GC (SEQ ID NO:32) and CTG TGA CCA TTG CTC CCA AGA GAG (SEQ ID NO:33), the promoter having the internal designation P15B4 (SEQ ID NO:34) was obtained.

Using the primer pairs CTG GGA TGG AAG GCA CGG TA (SEQ ID NO:35) and GAG ACC ACA CAG CTA GAC AA (SEQ ID NO:36), the promoter having the internal designation P29B6 (SEQ ID NO:37) was obtained.

Figure 7 provides a schematic description of the promoters isolated and the way they are assembled with the corresponding 5' tags. The upstream sequences were screened for the presence of motifs resembling transcription factor binding sites or known transcription start sites using the computer program MatInspector release 2.0, August 1996.

Figure 8 describes the transcription factor binding sites present in each of these promoters. The columns labeled matrices provides the name of the MatInspector matrix used. The column labeled position provides the 5' position of the promoter site. Numeration of the sequence starts from the transcription site as determined by matching the genomic sequence with the 5' EST sequence. The column labeled

"orientation" indicates the DNA strand on which the site is found, with the + strand being the coding strand as determined by matching the genomic sequence with the sequence of the 5' EST. The column labeled "score" provides the MatInspector score found for this site. The column labeled "length" provides the length of the site in nucleotides. The column labeled "sequence" provides the sequence of the site found.

The promoters and other regulatory sequences located upstream of the extended cDNAs or 5' ESTs may be used to design expression vectors capable of directing the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative manner. A promoter capable of directing the desired spatial, temporal, developmental, and quantitative patterns may be selected using the results of the expression analysis described in Example 26 above. For example, if a promoter which confers a high level of expression in muscle is desired, the promoter sequence upstream of an extended cDNA or 5' EST derived from an mRNA which is expressed at a high level in muscle, as determined by the method of Example 26, may be used in the expression vector.

Preferably, the desired promoter is placed near multiple restriction sites to facilitate the cloning of the desired insert downstream of the promoter, such that the promoter is able to drive expression of the inserted gene. The promoter may be inserted in conventional nucleic acid backbones designed for extrachromosomal replication, integration into the host chromosomes or transient expression. Suitable backbones for the present expression vectors include retroviral backbones, backbones from eukaryotic episomes such as SV40 or Bovine Papilloma Virus, backbones from bacterial episomes, or artificial chromosomes.

Preferably, the expression vectors also include a polyA signal downstream of the multiple restriction sites for directing the polyadenylation of mRNA transcribed from the gene inserted into the expression vector.

Following the identification of promoter sequences using the procedures of Examples 55-57, proteins which interact with the promoter may be identified as described in Example 58 below.

EXAMPLE 58

Identification of Proteins Which Interact with Promoter Sequences, Upstream Regulatory Sequences, or mRNA

Sequences within the promoter region which are likely to bind transcription factors may be identified by homology to known transcription factor binding sites or through conventional mutagenesis or deletion analyses of reporter plasmids containing the promoter sequence. For example, deletions may be made in a reporter plasmid containing the promoter sequence of interest operably linked to an assayable reporter gene. The reporter plasmids carrying various deletions within the promoter region are transfected into an appropriate host cell and the effects of the deletions on expression levels is assessed. Transcription factor binding sites within the regions in which deletions reduce expression levels may be further localized using site directed mutagenesis, linker scanning analysis, or other techniques familiar to those skilled in the

art. Nucleic acids encoding proteins which interact with sequences in the promoter may be identified using one-hybrid systems such as those described in the manual accompanying the Matchmaker One-Hybrid System kit available from Clontech (Catalog No. K1603-1). Briefly, the Matchmaker One-hybrid system is used as follows. The target sequence for which it is desired to identify binding proteins is cloned upstream of a selectable reporter gene and integrated into the yeast genome. Preferably, multiple copies of the target sequences are inserted into the reporter plasmid in tandem.

A library comprised of fusions between cDNAs to be evaluated for the ability to bind to the promoter and the activation domain of a yeast transcription factor, such as GAL4, is transformed into the yeast strain containing the integrated reporter sequence. The yeast are plated on selective media to select cells expressing the selectable marker linked to the promoter sequence. The colonies which grow on the selective media contain genes encoding proteins which bind the target sequence. The inserts in the genes encoding the fusion proteins are further characterized by sequencing. In addition, the inserts may be inserted into expression vectors or in vitro transcription vectors. Binding of the polypeptides encoded by the inserts to the promoter DNA may be confirmed by techniques familiar to those skilled in the art, such as gel shift analysis or DNase protection analysis.

VII. Use of Extended cDNAs (or Genomic DNAs Obtainable Therefrom) in Gene Therapy

The present invention also comprises the use of extended cDNAs (or genomic DNAs obtainable therefrom) in gene therapy strategies, including antisense and triple helix strategies as described in Examples 57 and 58 below. In antisense approaches, nucleic acid sequences complementary to an mRNA are hybridized to the mRNA intracellularly, thereby blocking the expression of the protein encoded by the mRNA. The antisense sequences may prevent gene expression through a variety of mechanisms. For example, the antisense sequences may inhibit the ability of ribosomes to translate the mRNA. Alternatively, the antisense sequences may block transport of the mRNA from the nucleus to the cytoplasm, thereby limiting the amount of mRNA available for translation. Another mechanism through which antisense sequences may inhibit gene expression is by interfering with mRNA splicing. In yet another strategy, the antisense nucleic acid may be incorporated in a ribozyme capable of specifically cleaving the target mRNA.

EXAMPLE 59

Preparation and Use of Antisense Oligonucleotides

The antisense nucleic acid molecules to be used in gene therapy may be either DNA or RNA sequences. They may comprise a sequence complementary to the sequence of the extended cDNA (or genomic DNA obtainable therefrom). The antisense nucleic acids should have a length and melting temperature sufficient to permit formation of an intracellular duplex having sufficient stability to inhibit the expression of the mRNA in the duplex. Strategies for designing antisense nucleic acids suitable for use in gene therapy are disclosed in Green et al., *Ann. Rev. Biochem.* **55**:569-597 (1986) and Izant and Weintraub, *Cell* **36**:1007-1015 (1984).

In some strategies, antisense molecules are obtained from a nucleotide sequence encoding a protein by reversing the orientation of the coding region with respect to a promoter so as to transcribe the opposite strand from that which is normally transcribed in the cell. The antisense molecules may be transcribed using in vitro transcription systems such as those which employ T7 or SP6 polymerase to generate the transcript. Another approach involves transcription of the antisense nucleic acids in vivo by operably linking DNA containing the antisense sequence to a promoter in an expression vector.

Alternatively, oligonucleotides which are complementary to the strand normally transcribed in the cell may be synthesized in vitro. Thus, the antisense nucleic acids are complementary to the corresponding mRNA and are capable of hybridizing to the mRNA to create a duplex. In some embodiments, the antisense sequences may contain modified sugar phosphate backbones to increase stability and make them less sensitive to RNase activity. Examples of modifications suitable for use in antisense strategies are described by Rossi et al., *Pharmacol. Ther.* **50(2)**:245-254 (1991).

Various types of antisense oligonucleotides complementary to the sequence of the extended cDNA (or genomic DNA obtainable therefrom) may be used. In one preferred embodiment, stable and semi-stable antisense oligonucleotides described in International Application No. PCT WO94/23026 are used. In these molecules, the 3' end or both the 3' and 5' ends are engaged in intramolecular hydrogen bonding between complementary base pairs. These molecules are better able to withstand exonuclease attacks and exhibit increased stability compared to conventional antisense oligonucleotides.

In another preferred embodiment, the antisense oligodeoxynucleotides against herpes simplex virus types 1 and 2 described in International Application No. WO 95/04141, are used.

In yet another preferred embodiment, the covalently cross-linked antisense oligonucleotides described in International Application No. WO 96/31523, are used. These double- or single-stranded oligonucleotides comprise one or more, respectively, inter- or intra-oligonucleotide covalent cross-linkages, wherein the linkage consists of an amide bond between a primary amine group of one strand and a carboxyl group of the other strand or of the same strand, respectively, the primary amine group being directly substituted in the 2' position of the strand nucleotide monosaccharide ring, and the carboxyl group being carried by an aliphatic spacer group substituted on a nucleotide or nucleotide analog of the other strand or the same strand, respectively.

The antisense oligodeoxynucleotides and oligonucleotides disclosed in International Application No. WO 92/18522, may also be used. These molecules are stable to degradation and contain at least one transcription control recognition sequence which binds to control proteins and are effective as decoys therefor. These molecules may contain "hairpin" structures, "dumbbell" structures, "modified dumbbell" structures, "cross-linked" decoy structures and "loop" structures.

In another preferred embodiment, the cyclic double-stranded oligonucleotides described in European Patent Application No. 0 572 287 A2 are used. These ligated oligonucleotide "dumbbells" contain the binding site for a transcription factor and inhibit expression of the gene under control of the

transcription factor by sequestering the factor.

Use of the closed antisense oligonucleotides disclosed in International Application No. WO 92/19732, is also contemplated. Because these molecules have no free ends, they are more resistant to degradation by exonucleases than are conventional oligonucleotides. These oligonucleotides may be multifunctional, interacting with several regions which are not adjacent to the target mRNA.

The appropriate level of antisense nucleic acids required to inhibit gene expression may be determined using in vitro expression analysis. The antisense molecule may be introduced into the cells by diffusion, injection, infection or transfection using procedures known in the art. For example, the antisense nucleic acids can be introduced into the body as a bare or naked oligonucleotide, oligonucleotide encapsulated in lipid, oligonucleotide sequence encapsulated by viral protein, or as an oligonucleotide operably linked to a promoter contained in an expression vector. The expression vector may be any of a variety of expression vectors known in the art, including retroviral or viral vectors, vectors capable of extrachromosomal replication, or integrating vectors. The vectors may be DNA or RNA.

The antisense molecules are introduced onto cell samples at a number of different concentrations preferably between 1×10^{-10} M to 1×10^{-4} M. Once the minimum concentration that can adequately control gene expression is identified, the optimized dose is translated into a dosage suitable for use in vivo. For example, an inhibiting concentration in culture of 1×10^{-7} translates into a dose of approximately 0.6 mg/kg bodyweight. Levels of oligonucleotide approaching 100 mg/kg bodyweight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the vertebrate are removed, treated with the antisense oligonucleotide, and reintroduced into the vertebrate.

It is further contemplated that the antisense oligonucleotide sequence is incorporated into a ribozyme sequence to enable the antisense to specifically bind and cleave its target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi et al., *supra*.

In a preferred application of this invention, the polypeptide encoded by the gene is first identified, so that the effectiveness of antisense inhibition on translation can be monitored using techniques that include but are not limited to antibody-mediated tests such as RIAs and ELISA, functional assays, or radiolabeling.

The extended cDNAs of the present invention (or genomic DNAs obtainable therefrom) may also be used in gene therapy approaches based on intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. They are particularly useful for studying alterations in cell activity as it is associated with a particular gene. The extended cDNAs (or genomic DNAs obtainable therefrom) of the present invention or, more preferably, a portion of those sequences, can be used to inhibit gene expression in individuals having diseases associated with expression of a particular gene. Similarly, a portion of the extended cDNA (or genomic DNA obtainable therefrom) can be used to study the effect of inhibiting transcription of a particular gene within a cell. Traditionally, homopurine

sequences were considered the most useful for triple helix strategies. However, homopyrimidine sequences can also inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at homopurine:homopyrimidine sequences. Thus, both types of sequences from the extended cDNA or from the gene corresponding to the extended cDNA are contemplated within the scope of this invention.

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EXAMPLE 60

Preparation and use of Triple Helix Probes

The sequences of the extended cDNAs (or genomic DNAs obtainable therefrom) are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches which could be used in triple-helix based strategies for inhibiting gene expression. Following identification of candidate homopyrimidine or homopurine stretches, their efficiency in inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into tissue culture cells which normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis, such as GENSET, Paris, France.

The oligonucleotides may be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

Treated cells are monitored for altered cell function or reduced gene expression using techniques such as Northern blotting, RNase protection assays, or PCR based strategies to monitor the transcription levels of the target gene in cells which have been treated with the oligonucleotide. The cell functions to be monitored are predicted based upon the homologies of the target gene corresponding to the extended cDNA from which the oligonucleotide was derived with known gene sequences that have been associated with a particular function. The cell functions can also be predicted based on the presence of abnormal physiologies within cells derived from individuals with a particular inherited disease, particularly when the extended cDNA is associated with the disease using techniques described in Example 53.

The oligonucleotides which are effective in inhibiting gene expression in tissue culture cells may then be introduced in vivo using the techniques described above and in Example 59 at a dosage calculated based on the in vitro results, as described in Example 59.

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases. Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3' end of the alpha oligonucleotide to stabilize the triple helix. For information on the generation of oligonucleotides suitable for triple helix formation see Griffin et al. *Science* **245**:967-971 (1989).

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EXAMPLE 61Use of Extended cDNAs to Express an Encoded Protein in a Host Organism

The extended cDNAs of the present invention may also be used to express an encoded protein in a host organism to produce a beneficial effect. In such procedures, the encoded protein may be transiently expressed in the host organism or stably expressed in the host organism. The encoded protein may have any of the activities described above. The encoded protein may be a protein which the host organism lacks or, alternatively, the encoded protein may augment the existing levels of the protein in the host organism.

A full length extended cDNA encoding the signal peptide and the mature protein, or an extended cDNA encoding only the mature protein is introduced into the host organism. The extended cDNA may be introduced into the host organism using a variety of techniques known to those of skill in the art. For example, the extended cDNA may be injected into the host organism as naked DNA such that the encoded protein is expressed in the host organism, thereby producing a beneficial effect.

Alternatively, the extended cDNA may be cloned into an expression vector downstream of a promoter which is active in the host organism. The expression vector may be any of the expression vectors designed for use in gene therapy, including viral or retroviral vectors.

The expression vector may be directly introduced into the host organism such that the encoded protein is expressed in the host organism to produce a beneficial effect. In another approach, the expression vector may be introduced into cells *in vitro*. Cells containing the expression vector are thereafter selected and introduced into the host organism, where they express the encoded protein to produce a beneficial effect.

EXAMPLE 62Use Of Signal Peptides Encoded By 5' Ests Or SequencesObtained Therefrom To Import Proteins Into Cells

The short core hydrophobic region (h) of signal peptides encoded by the 5'ESTS or extended cDNAs derived from the 5'ESTs of the present invention may also be used as a carrier to import a peptide or a protein of interest, so-called cargo, into tissue culture cells (Lin *et al.*, *J. Biol. Chem.*, **270**: 14225-14258 (1995); Du *et al.*, *J. Peptide Res.*, **51**: 235-243 (1998); Rojas *et al.*, *Nature Biotech.*, **16**: 370-375 (1998)).

When cell permeable peptides of limited size (approximately up to 25 amino acids) are to be translocated across cell membrane, chemical synthesis may be used in order to add the h region to either the C-terminus or the N-terminus to the cargo peptide of interest. Alternatively, when longer peptides or proteins are to be imported into cells, nucleic acids can be genetically engineered, using techniques familiar to those skilled in the art, in order to link the extended cDNA sequence encoding the h region to the 5' or the 3' end of a DNA sequence coding for a cargo polypeptide. Such genetically engineered nucleic acids are then translated either *in vitro* or *in vivo* after transfection into appropriate cells, using conventional

techniques to produce the resulting cell permeable polypeptide. Suitable hosts cells are then simply incubated with the cell permeable polypeptide which is then translocated across the membrane.

This method may be applied to study diverse intracellular functions and cellular processes. For instance, it has been used to probe functionally relevant domains of intracellular proteins and to examine protein-protein interactions involved in signal transduction pathways (Lin *et al.*, *supra*; Lin *et al.*, *J. Biol. Chem.*, **271**: 5305-5308 (1996); Rojas *et al.*, *J. Biol. Chem.*, **271**: 27456-27461 (1996); Liu *et al.*, *Proc. Natl. Acad. Sci. USA*, **93**: 11819-11824 (1996); Rojas *et al.*, *Bioch. Biophys. Res. Commun.*, **234**: 675-680 (1997)).

Such techniques may be used in cellular therapy to import proteins producing therapeutic effects. For instance, cells isolated from a patient may be treated with imported therapeutic proteins and then re-introduced into the host organism.

Alternatively, the h region of signal peptides of the present invention could be used in combination with a nuclear localization signal to deliver nucleic acids into cell nucleus. Such oligonucleotides may be antisense oligonucleotides or oligonucleotides designed to form triple helices, as described in examples 59 and 60 respectively, in order to inhibit processing and maturation of a target cellular RNA.

EXAMPLE 63

Reassembling & Resequencing of Clones

Further study of the clones reported in SEQ ID NOs: 40 to 86 revealed a series of abnormalities. As a result, the clones were resequenced twice, reanalyzed and the open reading frames were reassigned. The corrected nucleotide sequences have been disclosed in SEQ ID NOs: 134 to 180 and the predicted amino acid sequences for the corresponding polypeptides have also been corrected and disclosed in SEQ ID NOs: 181 to 227. The corrected sequences have been placed in the Sequence Listing in the same order as the original sequences from which they were derived.

After this reanalysis process a few apparent abnormalities persisted. The sequences presented in SEQ ID NOs: 134, 149, 151, and 164 are apparently unlikely to be genuine full length cDNAs. These clones are missing a stop codon and are thus more probably 3' truncated cDNA sequences. Similarly, the sequences presented in SEQ ID NOs: 145, 155, and 166 may also not be genuine full length cDNAs based on homology studies with existing protein sequences. Although both of these sequences encode a potential start methionine each could represent of 5' truncated cDNA.

In addition, after the reassignment of open reading frames for the clones, new open reading frames were chosen in some instances. In case of SEQ ID NOs: 135, 149, 155, 160, 166, 171, and 175 the new open reading frames were no longer predicted to contain a signal peptide.

Table VII provides the sequence identification numbers of the extended cDNAs of the present invention, the locations of the full coding sequences in SEQ ID NOs: 134-180 (i.e. the nucleotides encoding both the signal peptide and the mature protein, listed under the heading FCS location in Table VII), the

locations of the nucleotides in SEQ ID NOs: 134-180 which encode the signal peptides (listed under the heading SigPep Location in Table VII), the locations of the nucleotides in SEQ ID NOs: 134-180 which encode the mature proteins generated by cleavage of the signal peptides (listed under the heading Mature Polypeptide Location in Table VII), the locations in SEQ ID NOs: 134-180 of stop codons (listed under the heading Stop Codon Location in Table VII), the locations in SEQ ID NOs: 134-180 of polyA signals (listed under the heading PolyA Signal Location in Table VII) and the locations of polyA sites (listed under the heading PolyA Site Location in Table VII).

Table VIII lists the sequence identification numbers of the polypeptides of SEQ ID NOs: 181-227, the locations of the amino acid residues of SEQ ID NOs: 181-227 in the full length polypeptide (second column), the locations of the amino acid residues of SEQ ID NOs: 181-227 in the signal peptides (third column), and the locations of the amino acid residues of SEQ ID NOs: 181-227 in the mature polypeptide created by cleaving the signal peptide from the full length polypeptide (fourth column). In Table VIII, and in the appended sequence listing, the first amino acid of the mature protein resulting from cleavage of the signal peptide is designated as amino acid number 1 and the first amino acid of the signal peptide is designated with the appropriate negative number, in accordance with the regulations governing sequence listings.

EXAMPLE 64

Functional Analysis of Predicted Protein Sequences

Following double-sequencing, new contigs were assembled for each of the extended cDNAs of the present invention and each was compared to known sequences available at the time of filing. These sequences originate from the following databases : Genbank (release 108 and daily releases up to October, 15, 1998), Genseq (release 32) PIR (release 53) and Swissprot (release 35). The predicted proteins of the present invention matching known proteins were further classified into 3 categories depending on the level of homology.

It should be noted that the numbering of amino acids in the protein sequences discussed in Figures 9 to 16, and Table VI, the first methionine encountered is designated as amino acid number 1. In the appended sequence listing, the first amino acid of the mature protein resulting from cleavage of the signal peptide is designated as amino acid number 1 and the first amino acid of the signal peptide is designated with the appropriate negative number, in accordance with the regulations governing sequence listings.

The first category contains proteins of the present invention exhibiting more than 90% identical amino acid residues on the whole length of the matched protein. They are clearly close homologues which most probably have the same function or a very similar function as the matched protein.

The second category contains proteins of the present invention exhibiting more remote homologies (40 to 90% over the whole protein) indicating that the protein of the present invention is

susceptible to have functions similar to those of matched protein.

The third category contains proteins exhibiting high homology (90 to 100%) to a domain of a known protein indicating that the matched protein and the protein of the invention may share similar features.

In addition all of the corrected amino acid sequences (SEQ ID NOs: 181 to 227) were scanned for the presence of known protein signatures and motifs. This search was performed against the Prosite 34.0 database, using the Proscan software from the GCG package. Functional signatures and their locations are indicated in Table VI.

A) Proteins which are closely related to known proteins

Protein of SEQ ID NO: 214:

The protein of SEQ ID NO: 214 encoded by the extended cDNA SEQ ID NO: 167 isolated from brain shows extensive homology to a human SH3 binding domain glutamic acid-rich like protein or SH3BGRL (Egeo *et al*, *Biochem. Biophys. Res. Commun.*, **247**:302-306 (1998)) with Genbank accession number is AF042081. As shown by the alignments of Figure 9, the amino acid residues are identical except for positions 63 and 101 in the 114 amino acid long matched sequence. This SH3BGRL protein is itself homologous to the middle proline-rich region of a protein containing an SH3 binding domain, the SH3BGR protein (Scartezzini *et al.*, *Hum. Genet.*, **99**:387-392 (1997)). This proline-rich region is also highly conserved in mice. Both SH3BGR and SH3BGRL proteins are thought to be involved in the Down syndrome pathogenesis. The protein SEQ ID NO: 214 also contains the proline-rich SH3 binding domain (bold) and a potential RGD cell attachment sequence (underlined).

SH3 domains are small important functional modules found in several proteins from all eukaryotic organisms that are involved in a whole range of regulation of protein-protein interaction, e.g. in regulating enzymatic activities, recruiting specific substrates to the enzyme in signal transduction pathways, in interacting with viral proteins and they are also thought to play a role in determining the localization of proteins to the plasma membrane or the cytoskeleton (for a review, see Cohen *et al*, *Cell*, **80**:237-248 (1995)).

The Arg-Gly-Asp (RGD) attachment site promote cell adhesion of a large number of adhesive extracellular matrix, blood and cell surface proteins to their integrin receptors which have been shown to regulate cell migration, growth, differentiation and apoptosis. This cell adhesion activity is also maintained in short RGD containing synthetic peptides which were shown to exhibit anti-thrombolytic and anti-metastatic activities and to inhibit bone degradation *in vivo* (for review, see Ruoslahti, *Annu. Rev. Cell Dev. Biol.*, **12**:697-715 (1996)).

Taken together, these data suggest that the protein of SEQ ID NO: 214 may be important in regulating protein-protein interaction in signal transduction pathways, and/or may play a role of localization of proteins to the plasma membrane or cytoskeleton, and/or may play a role in cell adhesion. Moreover, this protein or part therein, especially peptides containing the RGD motif, may be useful in

diagnosing and treating cancer, thrombosis, osteoporosis and/or in diagnosing and treating disorders associated with the Down syndrome.

Proteins of SEQ ID NOs: 185 and 215:

The nearly homologous proteins of SEQ ID NOs: 185 and 215 encoded by the extended cDNA
 5 SEQ ID NOs: 138 and 168, respectively, exhibit an extensive homology with a murine protein named
 MP1 for MEK binding partner 1 (Genbank accession number AF082526). The amino acid residues are
 identical to the murine protein except for positions 39, 118 and 119 of the Genbank MP1 sequence for
 SEQ ID NO: 215 and except for positions 33, 39, 118 and 119 of the Genbank MP1 sequence for SEQ ID
 NO: 185. The Genbank MP1 sequence is the 124 amino acid long matched protein region. See the
 10 amino acid sequence alignment in Figure 10. MP1 was shown to enhance enzymatic activation of
 mitogen-activated protein (MAP) kinase cascade. The MAP kinase pathway is one of the important
 enzymatic cascade that is conserved among all eukaryotes from yeast to human. This kind of pathway is
 involved in vital functions such as the regulation of growth, differentiation and apoptosis. MP1 probably
 acts by facilitating the interaction of the two sequentially acting kinases MEK1 and ERK1 (Schaffer *et*
 15 *al.*, *Science*, **281**:1668-1671 (1998)).

Taken together, these data suggest that the proteins of SEQ ID NO: 185 and 215 may be involved
 in regulating protein-protein interaction in the signal transduction pathways. Thus, these proteins may be
 useful in diagnosing and/or treating several types of disorders including, but not limited to, cancer,
 neurodegenerative diseases, cardiovascular disorders, hypertension, renal injury and repair and septic
 20 shock.

Protein of SEQ ID NO: 186

The protein of SEQ ID NO: 186 encoded by the extended cDNA SEQ ID NO: 139 exhibits an
 extensive homology with a murine protein named claudin-2 (Genbank accession number AF072128).
 The amino acid residues are identical except for the conservative substitutions observed at positions: 6,
 25 22, 23, 29, 31, 90, 110, 120, 130, 171, 176, 179, 187, 192, 197, 211, 212, 214, and 217 of the 230 amino
 acids long matched protein claudin-2. One drastic substitution from glycine to arginine was observed at
 position 189. See the amino acid sequence alignment in Figure 11. The murine homologue claudin-2 is
 a integral membrane proteins with 4 putative transmembrane domains belonging to a family of proteins
 thought to be involved in the formation of tight junctions between cells in epithelial or endothelial cell
 30 sheets (Furuse *et al.*, *J. Cell. Biol.*, **141**:1539-1550, (1998)).

In addition, the protein of SEQ ID NO: 186 shows more remote homology to a family of
 transmembrane proteins among which are receptors for *Clostridium perfringens* enterotoxin (CPE) with
 either high or low affinity for CPE (Katahira *et al.*, *J. Biol. Chem.*, **452**:26652-26658 (1997)). The
 matched region include the 4 putative transmembrane regions.

35 Taken together, these data suggest that the protein of SEQ ID NO: 186 may be involved in the
 formation and/or regulation of tight junction, and more generally in cell-cell adhesion. This protein may

also function as a receptor for a yet unknown ligand that may show homology to CPE. This protein may thus be useful in diagnosing and/or treating disorders associated with changes in epithelium permeability such as infectious diseases caused by *Clostridium* parasites.

Protein of SEQ ID NO: 213

The protein of SEQ ID NO: 213 encoded by the extended cDNA SEQ ID NO: 166 and expressed in lymphocytes exhibits an extensive homology to a stretch of 121 amino acid of a human hematopoietic maturation factor named glia maturation factor gamma or GMF- γ (Genbank accession number AB001993) and also to other glia maturation factors found in human, bovine and rodent species. The amino acid residues are identical as shown below except for conservative substitutions at positions 50, and 77 of the 142 amino acids long matched protein GMF- γ which is itself highly homologous to GMF- β (Asai *et al.*, *Biochem. Biophys. Acta*, **1396**:242-244 (1998)). See the amino acid sequence alignment in Figure 12. GMF- β was shown to act as a growth and differentiation factor for neurons and glial cells in human brain (Lim *et al.*, *Proc Natl Acad Sci U S A* **86**:3901-3905 (1989); and Harman *et al.*, *Brain Res.* **56**:332-335 (1991)) and is also thought to regulate ERK proteins of the evolutionarily conserved mitogen-activated protein (MAP) kinase cascade which is important in the regulation of growth, differentiation and apoptosis (Zaheer and Lim, *J. Biol. Chem.*, **272**:5183-5186 (1997)).

Taken together, these data suggest that the protein of SEQ ID NO: 213 may be involved in cell growth and differentiation and/or in apoptosis and/or in intracellular signaling. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limiting to, cancer, neurodegenerative diseases, cardiovascular disorders, hypertension, renal injury and repair and septic shock.

Protein of SEQ ID NO: 191

The protein of SEQ ID NO: 191 encoded by the extended cDNA SEQ ID NO: 144 and expressed in lymphocytes exhibits an extensive homology to a stretch of 91 amino acid of a human secreted protein expressed in peripheral blood mononucleocytes (Genpep accession number W36955 and Genseq accession number VOO433). The amino acid residues are identical except for the substitution of asparagine to isoleucine at positions 94, and the conservative substitutions at positions 108, 109 and 110 of the 110 amino acids long matched protein. See the amino acid sequence alignment in Figure 13.

Protein of SEQ ID NO: 200

The protein of SEQ ID NO: 200 encoded by the extended cDNA SEQ ID NO: 153 exhibits extensive homologies to proteins encoding RING zinc finger proteins of the human, chicken and rodent species, as well as an EGF-like domain. Two stretches of 341 and of 13 amino acids of the human RING zinc finger protein which might bind DNA (Genbank accession number AF037204). The amino acid residues are identical except for conservative substitutions at positions 18, 29, 156 and 282 of the 381 amino acid long human RING zinc finger. See the amino acid sequence alignment in Figure 14. Such RING zinc finger proteins are thought to be involved in protein-protein interaction and are especially

found in nucleic acid binding proteins. Secreted proteins may have nucleic acid binding domain as shown by a nematode protein thought to regulate gene expression which exhibits zinc fingers as well as a functional signal peptide (Holst and Zipfel, *J. Biol. Chem.*, **271**:16275-16733 (1996)).

Taken together, these data suggest that the protein of SEQ ID NO: 200 may play a role in protein-protein interaction or be a nucleic acid binding protein.

Protein of SEQ ID NO: 192

The protein of SEQ ID NO: 192 encoded by the extended cDNA SEQ ID NO: 145 exhibits extensive homologies to stretches of proteins encoding vacuolar proton-ATPase subunits M9.2 of either human (Genbank accession number Y15286) or bovine species (Genbank accession number Y15285). These two highly conserved proteins are extremely hydrophobic membrane proteins with two membrane-spanning helices and a potential metal-binding domain conserved in mammalian protein homologues (Ludwig *et al.*, *J. Biol. Chem.*, **273**:10939-10947 (1998)). The amino acid residues are completely identical as shown in the alignment in Figure 15. However, the protein of SEQ ID NO: 192 is missing amino acids 1 to 92 from the Genbank sequences. The protein of SEQ ID NO: 192 contains the second putative transmembrane domain as well as the potential metal-binding site.

Taken together, these data suggest that the protein of SEQ ID NO: 192 may play a role in energy conservation, secondary active transport, acidification of intracellular compartments and/or cellular pH homeostasis.

B) Proteins which are remotely related to proteins with known functions

Proteins of SEQ ID NOs: 201 and 227

The proteins of SEQ ID NOs: 201 and 227 encoded by the extended cDNA SEQ ID NOs: 154 and 180, respectively, belong to the stomatin or band 7 family. The human stomatin is an integral membrane phosphoprotein thought to be involved to regulate the cation conductance by interacting with other proteins of the junctional complex of the membrane skeleton (Gallagher and Forget, *J. Biol. Chem.*, **270**:26358-26363 (1995)). The proteins of SEQ ID NOs: 201 and 227 exhibit the PROSITE signature typical for the band 7 family signature. See the amino acid sequence alignment in Figure 16.

Taken together, these data suggest that the proteins of SEQ ID NOs: 201 and 227 play a role in the regulation of ion transport, hence in the control of cellular volume. These proteins may then be useful in diagnosing and/or treating stomatocytosis and/or cryohydrocytosis.

Protein of SEQ ID NO: 198

The protein of SEQ ID NO: 198 encoded by the extended cDNA SEQ ID NO: 151 shows homologies with different DNA or RNA binding proteins such as the human Staf50 transcription factor (Genbank accession number X82200), the human Ro/SS-A ribonucleoprotein autoantigen (Swissprot accession number P19474) or the murine RPT1 transcription factor (Swissprot accession number P15533). The protein of SEQ ID NO: 198 exhibits a putative signal peptide and also a PROSITE signature for a RING type zinc finger domain located from positions 15 to 59. Secreted proteins may

have nucleic acid binding domain as shown by a nematode protein thought to regulate gene expression which exhibits zinc fingers as well as a functional signal peptide (Holst and Zipfel, *J. Biol. Chem.*, **271**:16275-16733 (1996)).

Taken together, these data suggest that the protein of SEQ ID NO: 198 may play a role in protein-protein interaction in intracellular signaling and eventually may directly or indirectly bind to DNA and/or RNA, hence regulating gene expression.

Protein of SEQ ID NO: 216

The protein of SEQ ID NO: 216 found in testis encoded by the extended cDNA SEQ ID NO: 169 shows homologies to protein domains with a 4-disulfide core signature found in either an extracellular proteinase inhibitor named chelonianin (Swissprot accession number P00993) or in rabbit and human proteins specifically expressed in epididymes (Genbank accession numbers U26725 and R13329). The matched domain in red sea turtle chelonianin is known to inhibit subtilisin, a serine protease (Kato and Tominaga, *Fed. Proc.*, **38**:832 (1979)). All cysteines of the 4 disulfide core signature thought to be crucial for biological activity are present in the protein of SEQ ID NO: 216. The 4 disulfide core signature is present except for a conservative substitution of asparagine to glutamine.

Taken together, these data suggest that the protein of SEQ ID NO: 216 may play a role in protein-protein interaction, act as a protease inhibitor and/or may also be related to male fertility .

Protein of SEQ ID NO: 197

The protein of SEQ ID NO: 197 encoded by the extended cDNA SEQ ID NO: 150 shows extensive homology to the connexin family conserved in the rodent, chicken, human, frog, sheep species. Connexins are a family of integral membrane proteins that oligomerize into clusters of intercellular channels called gap junctions, which join cells in virtually all metazoans. These channels permit exchange of ions between neurons and between neurons and excitable cells such as myocytes (for review, see Goodenough *et al.*, *Ann. Rev. Biochem.*, **65**:475-502 (1996)).

Taken together, these data suggest that the protein of SEQ ID NO: 197 may play a role in cell growth, differentiation and developmental signaling. Moreover, the protein of SEQ ID NO: 197 may be useful in diagnosing and/or treating cancer, neurodegenerative diseases and cardiovascular disorders.

C) Proteins homologous to a domain of a protein with known function

Protein of SEQ ID NO: 183

The protein of SEQ ID NO: 183 encoded by the extended cDNA SEQ ID NO: 136 shows homology to a rabbit soluble protein called PiUS (Genbank accession number U74297) which is a stimulator of inorganic phosphate uptake and is thought to be involved in cellular phosphate metabolism and/or binding (Norbis *et al.*, *J. Memb. Biol.*, **156**:19-24 (1997)).

Taken together, these data suggest that the protein of SEQ ID NO: 183 may play a role in

phosphate metabolism.

Protein of SEQ ID NO: 223

The protein of SEQ ID NO: 223 encoded by the extended cDNA SEQ ID NO: 176 shows homology to short stretches of a human protein called Tspan-1 (Genbank accession number AF054838) which belongs to the 4 transmembrane superfamily of molecular facilitators called tetraspanin (Meakers *et al.*, *FASEB J.*, **11**:428-442 (1997)).

Taken together, these data suggest that the protein of SEQ ID NO: 223 may play a role in cell activation and proliferation, and/or adhesion and motility and/or differentiation and cancer.

Protein of SEQ ID NO: 193

The protein of SEQ ID NO: 193 encoded by the extended cDNA SEQ ID NO: 146 shows homology to short stretches of *Drosophila*, *C. elegans* and chloroplast proteins similar to *E. coli* ribosomal protein L16.

Taken together, these data suggest that the protein of SEQ ID NO: 193 may be a ribosomal protein.

As discussed above, the extended cDNAs of the present invention or portions thereof can be used for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination for expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris *et al.*, *Cell* **75**:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins or polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative

receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

5 Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation *Molecular Cloning; A Laboratory Manual*, 2d ed., Cole Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., (1989), and *Methods in*
10 *Enzymology; Guide to Molecular Cloning Techniques*, Academic Press, Berger, S.L. and A.R. Kimmel eds., (1987).

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or
15 polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Although this invention has been described in terms of certain preferred embodiments, other
20 embodiments which will be apparent to those of ordinary skill in the art in view of the disclosure herein are also within the scope of this invention. Accordingly, the scope of the invention is intended to be defined only by reference to the appended claims. Throughout this application, various publications, patents, and published patent applications are cited.

The disclosures of the publications, patents, and published patent specifications referenced in
25 this application are hereby incorporated by reference into the present disclosure to more fully describe the state of the art to which this invention pertains.

Step	Search Characteristics			Selection Characteristics	
	Program	Strand	Parameters	Identity (%)	Length (bp)
Miscellaneous	blastn	both	S=61 X=16	90	17
tRNA	fasta	both	-	80	60
rRNA	blastn	both	S=108	80	40
mtRNA	blastn	both	S=108	80	40
Procaryotic	blastn	both	S=144	90	40
Fungal	blastn	both	S=144	90	40
Alu	fasta*	both	-	70	40
L1	blastn	both	S=72	70	40
Repeats	blastn	both	S=72	70	40
Promoters	blastn	top	S=54 X=16	90	15†
Vertebrate	fasta*	both	S=108	90	30
ESTs	blastn	both	S=108 X=16	90	30
Proteins	blastx◇	top	E=0.001	-	-

Table 1: Parameters used for each step of EST analysis

* use "Quick Fast" Database Scanner

† alignment further constrained to begin closer than 10bp to EST \ 5' end

◇ using BLOSUM62 substitution matrix

TABLE II

Id	FCS Location	SigPep Location	Mature Polypeptide Location	Stop Codon Location	PolyA Signal Location	PolyA Site Location
40	173-565	173-211	212-565	566	1063-1068	1087-1098
41	267-455	267-371	372-455	456	817-822	842-855
42	174-662	174-266	267-662	663	1144-1149	1165-1176
43	460-615	460-555	556-615	616	614-619	635-648
44	79-450	79-369	370-450	451	1217-1222	1240-1251
45	160-849	160-231	232-849	850	1510-1515	1506-1519
46	106-321	106-201	202-321	322	577-582	598-610
47	359-631	359-466	467-631	632	1334-1339	1357-1370
48	191-508	191-286	287-508	509	755-760	780-791
49	346-861	346-408	409-861	862	1400-1405	1420-1433
50	214-381	214-339	340-381	382	1133-1138	1146-1158
51	372-509	372-437	438-509	510	812-817	838-850
52	132-884	132-215	216-884	885	1069-1074	1094-1107
53	199-429	199-288	289-429	430	464-469	489-500
54	293-535	293-385	386-535	536	733-738	752-765
55	130-507	130-189	190-507	508	546-551	572-584
56	191-1009	191-325	326-1009	1010	1348-1353	1374-1387
57	141-614	141-251	252-614	615	1354-1359	1375-1385
58	212-364	212-268	269-364	365	1465-1470	1489-1497
59	147-1223	147-248	249-1223	1224	1538-1543	1558-1570
60	112-984	112-237	238-984	985	976-981	1010-1022
61	239-439	239-316	317-439	440	586-591	603-615
62	157-537	157-345	346-537	538	771-776	791-804
63	194-484	194-253	254-484	485	768-773	780-792
64	148-405	148-207	208-405	406	789-794	820-832
65	156-368	156-230	231-368	369	706-711	709-721
66	272-451	272-397	398-451	452	503-508	518-531
67	381-734	381-629	630-734	735	736-741	770-783
68	140-367	140-205	206-367	368	965-970	984-996
69	183-467	183-338	339-467	468	620-625	644-657
70	140-385	140-205	206-385	386	383-388	405-416
71	129-395	129-176	177-395	396	513-518	530-543
72	285-374	285-341	342-374	375	575-580	592-605
73	136-480	136-444	445-480	481	835-840	851-864
74	200-514	200-427	428-514	515	1001-1006	1022-1033
75	68-346	68-133	134-346	347	472-477	490-499
76	274-600	274-399	400-600	601	943-948	966-978
77	421-573	421-465	466-573	574	553-558	575-587
78	198-365	198-278	279-365	366	364-369	387-400
79	167-652	167-229	230-652	653	1133-1138	1154-1166

TABLE2:ss
111397

TABLE III

Id	Motif Location	Motif
55	160-226	Zinc finger, C2H2 type, domain
56	683-734	Connexins signatures
57	231-261	Zinc finger, C3HC4 type, signature

TABLE3:ss
111397

TABLE3:ss
111397

TABLE IV

Id	Full Length Polypeptide Location	Signal Peptide Location	Mature Polypeptide Location
87	1-131	1-13	14-131
88	1-63	1-35	36-63
89	1-163	1-31	32-163
90	1-52	1-32	33-52
91	1-124	1-97	98-124
92	1-230	1-24	25-230
93	1-72	1-32	33-72
94	1-91	1-36	37-91
95	1-106	1-32	33-106
96	1-172	1-21	22-172
97	1-56	1-42	43-56
98	1-46	1-22	23-46
99	1-251	1-28	29-251
100	1-77	1-30	31-77
101	1-81	1-31	32-81
102	1-126	1-20	21-126
103	1-273	1-45	46-273
104	1-158	1-37	38-158
105	1-51	1-19	20-51
106	1-359	1-34	35-359
107	1-291	1-42	43-291
108	1-67	1-26	27-67
109	1-127	1-63	64-127
110	1-97	1-20	21-97
111	1-86	1-20	21-86
112	1-71	1-25	26-71
113	1-60	1-42	43-60
114	1-118	1-83	84-118
115	1-76	1-22	23-76
116	1-95	1-52	53-95
117	1-82	1-22	23-82
118	1-89	1-16	17-89
119	1-30	1-19	20-30
120	1-115	1-103	104-115
121	1-105	1-76	77-105
122	1-93	1-22	23-93
123	1-109	1-42	43-109

Id	Full Length Polypeptide Location	Signal Peptide Location	Mature Polypeptide Location
124	1-51	1-15	16-51
125	1-56	1-27	28-56
126	1-162	1-21	22-162
127	1-126	1-68	69-126
128	1-140	1-40	41-140
129	1-43	1-24	25-43
130	1-69	1-21	22-69
131	1-78	1-19	20-78
132	1-80	1-47	48-80
133	1-53	1-42	43-53

TABLE4:ss
111397

TABLE V

Id	No-matches	Est <30%	Est >30%	Vrt
40			X	
41		X		
42			X	
43	X			
44			X	
45		X		
46			X	
47		X		
48			X	
49			X	
50		X		
51			X	
52			X	
53			X	
54			X	
55	X			
56			X	
57		X		
58			X	
59			X	
60	X			
61			X	
62			X	
63			X	
64			X	
65			X	
66			X	
67		X		
68			X	
69		X		
70		X		
71			X	
72				X
73			X	
74			X	
75	X			
76			X	
77			X	
78	X			

Id	No-matches	Est <30%	Est >30%	Vrt
79			X	
80			X	
81			X	
82			X	
83			X	
84			X	
85			X	
86	X			

TABLE5:ss
111397

TABLE5:ss
111397

- PROTEIN SIGNATURE -

SEQ ID	LOCATION	MOTIF
214	76 - 78	cell attachment site
	32 - 53	Leucine zipper
201	289 - 291	Microbodies C-terminal targeting signal
	164 - 192	Band 7 protein family
227	239 - 241	Microbodies C-terminal targeting signal
	114 - 142	Band 7 protein family
205	179 - 182	Endoplasmic reticulum targeting signal
226	78 - 81	Microbodies C-terminal targeting signal
181	99 - 101	cell attachment site
200	264 - 278	EGF like domain
	240 - 282	C3HC4 zinc finger (RING finger)
196	10 - 32	C2H2 zinc finger
198	15 - 59	C3HC4 zinc finger (RING finger)
218	21 - 42	Leucine zipper
197	164 - 180	connexins

TABLE VI

Table VII

SEQ ID	FCS Location	SigPep Location	Mature Polypeptide Location	Stop Codon Location	PolyA Signal Location	PolyA Site Location
134	131/1042	131/169	170/1042	-	-	1042/1053
135	100/276	-	100/276	277	638/643	662/675
136	111/401	111/194	195/401	402	1080/1085	1101/1112
137	359/514	359/454	455/514	515	-	536/547
138	26/397	26/316	317/397	398	1164/1169	1187/1198
139	36/725	36/107	108/725	726	1302/1307	1389/1400
140	35/250	35/130	131/250	251	505/510	526/538
141	169/432	169/267	268/432	433	1132/1137	1155/1167
142	143/460	143/238	239/460	461	697/702	721/730
143	108/908	108/170	171/908	909	1141/1146	1161/1174
144	209/532	-	209/532	533	1133/1138	1146/1158
145	5/211	5/142	143/211	212	716/721	742/754
146	98/850	98/181	182/850	851	1035/1040	1060/1073
147	46/342	46/189	190/342	343	377/382	402/413
148	139/381	139/231	232/381	382	579/584	598/609
149	72/512	-	72/512	-	-	512/522
150	126/944	126/260	261/944	945	1283/1288	1309/1322
151	50/1279	50/160	161/1279	-	-	1280/1290
152	83/1261	83/139	140/1261	1262	-	1356/1354
153	57/1199	57/95	96/1199	1200	1438/1443	1458/1470
154	72/944	72/197	198/944	945	-	970/982
155	4/279	-	4/279	280	425/430	443/455
156	90/470	90/278	279/470	471	704/709	724/738
157	88/339	88/147	148/339	340	619/624	637/649
158	33/578	33/92	93/578	579	-	703/714
159	33/245	33/107	108/245	246	546/551	584/596
160	125/343	-	125/343	344	375/380	390/403
161	126/632	126/575	576/632	633	670/675	721/727
162	90/317	90/155	156/317	318	913/918	932/944
163	126/410	126/287	288/410	411	561/566	587/598
164	85/348	85/150	151/348	-	-	349/360
165	77/343	77/124	125/343	344	461/466	477/490
166	38/364	-	38/364	365	458/463	475/488
167	48/389	48/356	357/389	390	742/747	760/771
168	69/440	69/359	360/440	441	927/932	947/959
169	33/311	33/98	99/311	312	437/442	455/464
170	110/730	110/235	236/730	731	764/769	787/799
171	38/214	-	38/214	215	-	308/320
172	129/296	129/209	210/296	297	-	318/331
173	78/563	78/359	360/563	564	1042/1047	1063/1075
174	62/523	62/265	266/523	524	602/607	621/632
175	24/320	-	24/320	321	402/407	419/430
176	42/170	42/113	114/170	171	-	172/185
177	108/314	108/170	171/314	315	550/555	574/585
178	118/351	118/171	172/351	352	583/588	602/613
179	128/367	128/268	269/367	368	410/415	424/427
180	149/871	149/457	458/871	872	-	893/912

Table VIII

SEQ ID	Full Length Polypeptide Location	Signal Peptide Location	Mature Polypeptide Location
134	-13/291	-13/-1	1/291
135	1/59	-	1/59
136	-28/69	-28/-1	1/69
137	-32/20	-32/-1	1/20
138	-97/27	-97/-1	1/27
139	-24/206	-24/-1	1/206
140	-32/40	-32/-1	1/40
141	-33/55	-33/-1	1/55
142	-32/74	-32/-1	1/74
143	-21/246	-21/-1	1/246
144	1/108	-	1/108
145	-46/23	-46/-1	1/23
146	-28/223	-28/-1	1/223
147	-48/51	-48/-1	1/51
148	-31/50	-31/-1	1/50
149	1/147	-	1/147
150	-45/228	-45/-1	1/228
151	-37/373	-37/-1	1/373
152	-19/374	-19/-1	1/374
153	-13/368	-13/-1	1/368
154	-42/249	-42/-1	1/249
155	1/92	-	1/92
156	-63/64	-63/-1	1/64
157	-20/64	-20/-1	1/64
158	-20/162	-20/-1	1/162
159	-25/46	-25/-1	1/46
160	1/73	-	1/73
161	-150/19	-150/-1	1/19
162	-22/54	-22/-1	1/54
163	-54/41	-54/-1	1/41
164	-22/66	-22/-1	1/66
165	-16/73	-16/-1	1/73
166	1/109	-	1/109
167	-103/11	-103/-1	1/11
168	-97/27	-97/-1	1/27
169	-22/71	-22/-1	1/71
170	-42/165	-42/-1	1/165
171	1/59	-	1/59
172	-27/29	-27/-1	1/29
173	-94/68	-94/-1	1/68
174	-68/86	-68/-1	1/86
175	1/99	-	1/99
176	-24/19	-24/-1	1/19
177	-21/48	-21/-1	1/48
178	-18/60	-18/-1	1/60
179	-47/33	-47/-1	1/33
180	-103/138	-103/-1	1/138
180	-103/138	-103/-1	1/138

CLAIMS**What Is Claimed Is:**

1. A purified or isolated nucleic acid comprising the sequence of one of SEQ ID NOs: 134-180 or a sequence complementary thereto.
- 5 2. A purified or isolated nucleic acid comprising at least 10 consecutive bases of the sequence of one of SEQ ID NOs: 134-180 or one of the sequences complementary thereto.
3. A purified or isolated nucleic acid comprising the full coding sequences of one of SEQ ID NOs: 136-148, 150, 152-154, 156-159, 161-163, 165, 167-170, 172-174, and 176-180, wherein the full coding sequence comprises the sequence encoding signal peptide and the sequence
10 encoding mature protein.
4. A purified or isolated nucleic acid comprising the nucleotides of one of SEQ ID NOs: 135-148, 150, 152-163, and 165-180 which encode a mature protein.
5. A purified or isolated nucleic acid comprising the nucleotides of one of SEQ ID NOs: 134, 136-148, 150-154, 156-159, 161-165, 167-170, 172-174, and 176-180 which encode the
15 signal peptide.
6. A purified or isolated nucleic acid encoding a polypeptide having the sequence of one of the sequences of SEQ ID NOs: 181-227.
7. A purified or isolated nucleic acid encoding a polypeptide having the sequence of a mature protein included in one of the sequences of SEQ ID NOs: 182-195, 197, 199-210, and 212-
20 227.
8. A purified or isolated nucleic acid encoding a polypeptide having the sequence of a signal peptide included in one of the sequences of SEQ ID NOs: 181, 183-195, 197-201, 203-206, 208-212, 214-217, 219-221, and 223-227.
9. A purified or isolated protein comprising the sequence of one of SEQ ID NOs:
25 181-227.
10. A purified or isolated polypeptide comprising at least 10 consecutive amino acids of one of the sequences of SEQ ID NOs: 181-227.
11. An isolated or purified polypeptide comprising a signal peptide of one of the polypeptides of SEQ ID NOs: 181, 183-195, 197-201, 203-206, 208-212, 214-217, 219-221, and
30 223-227.
12. An isolated or purified polypeptide comprising a mature protein of one of the polypeptides of SEQ ID NOs: 182-195, 197, 199-210, and 212-227.
13. A method of making a protein comprising one of the sequences of SEQ ID NO:

181-227, comprising the steps of:

obtaining a cDNA comprising one of the sequences of sequence of SEQ ID NO: 134-180;

inserting said cDNA in an expression vector such that said cDNA is operably linked to a promoter; and

5 introducing said expression vector into a host cell whereby said host cell produces the protein encoded by said cDNA.

14. The method of Claim 13, further comprising the step of isolating said protein.

15. A protein obtainable by the method of Claim 14.

16. A host cell containing a recombinant nucleic acid of Claim 1.

10 17. A purified or isolated antibody capable of specifically binding to a protein having the sequence of one of SEQ ID NOs: 181-227.

18. In an array of polynucleotides of at least 15 nucleotides in length, the improvement comprising inclusion in said array of at least one of the sequences of SEQ ID NOs: 134-180, or one of the sequences complementary to the sequences of SEQ ID NOs: 134-180, or a fragment thereof
15 of at least 15 consecutive nucleotides.

112

Abstract of the Disclosure

10

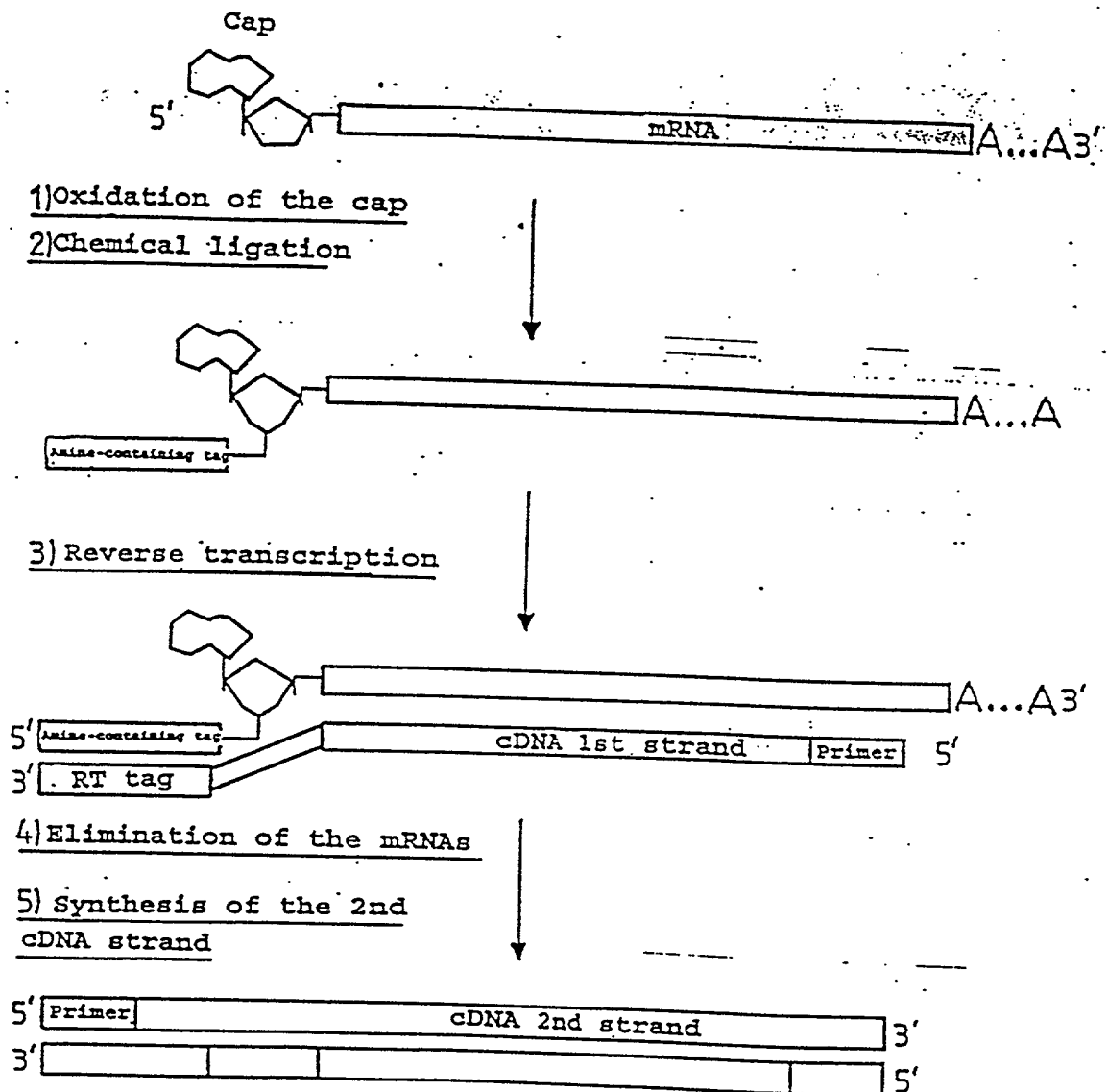


FIGURE 1

Minimum signal peptide score	false positive rate	false negative rate	proba(0.1)	proba(0.2)
3,5	0,121	0,036	0,467	0,664
4	0,096	0,06	0,519	0,708
4,5	0,078	0,079	0,565	0,745
5	0,062	0,098	0,616	0,782
5,5	0,05	0,127	0,659	0,813
6	0,04	0,163	0,694	0,836
6,5	0,033	0,202	0,725	0,855
7	0,025	0,248	0,763	0,878
7,5	0,021	0,304	0,78	0,889
8	0,015	0,368	0,816	0,909
8,5	0,012	0,418	0,836	0,92
9	0,009	0,512	0,856	0,93
9,5	0,007	0,581	0,863	0,934
10	0,006	0,678	0,835	0,919

FIGURE 2

Score curves

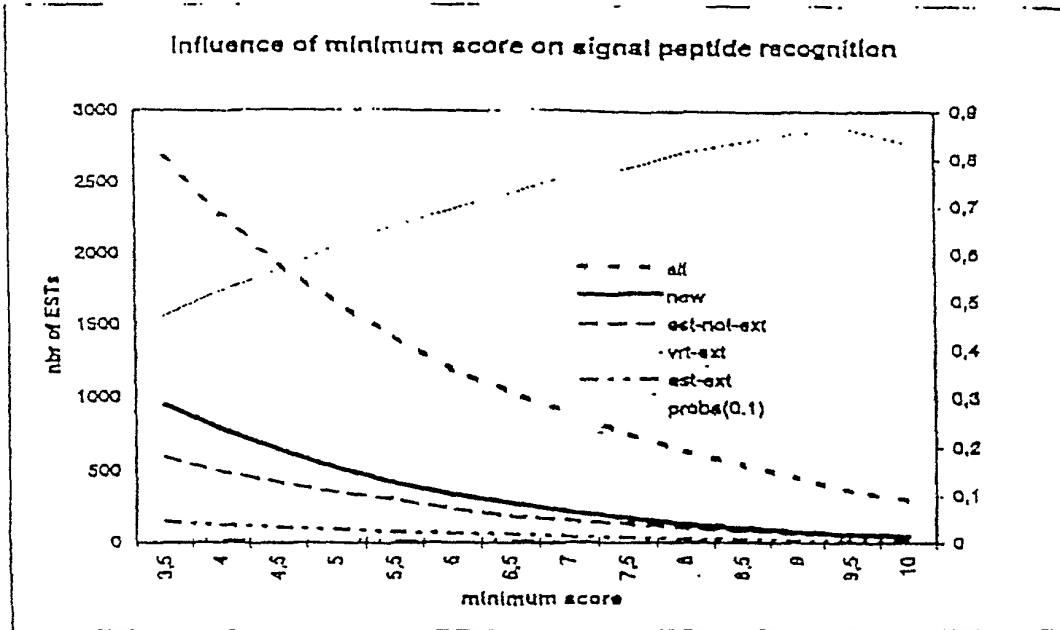


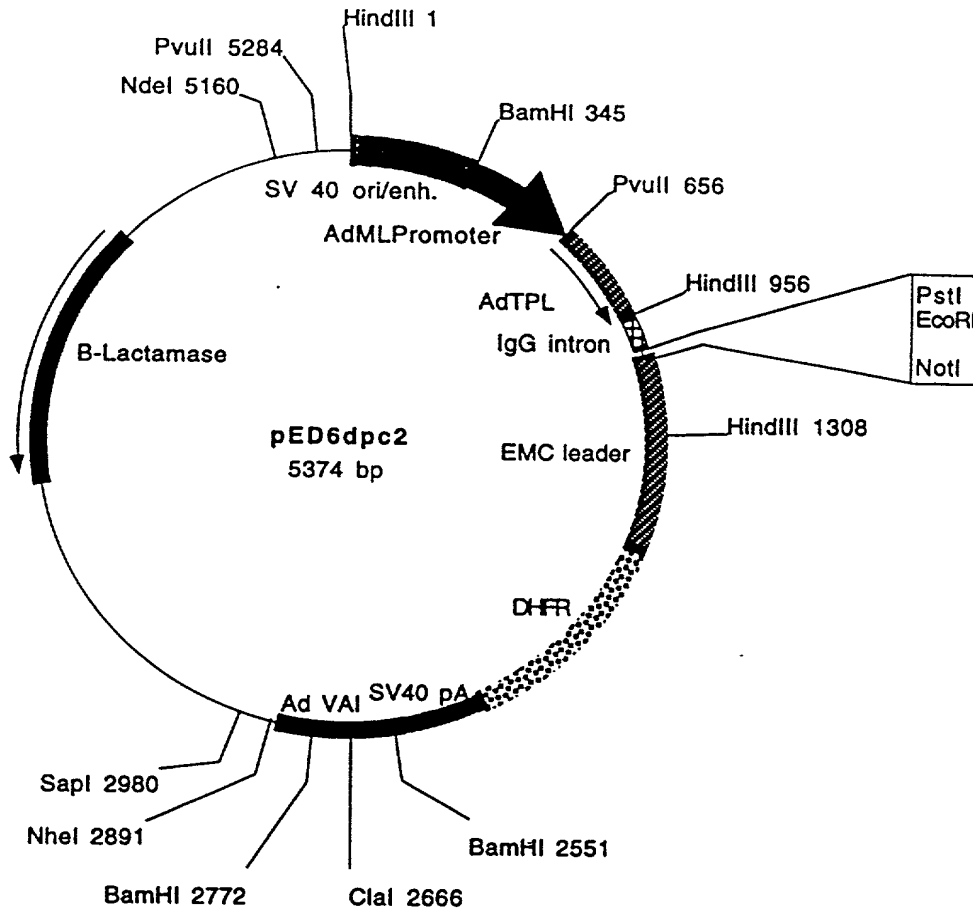
FIGURE 3

Minimum signal peptide score	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
3,5	2874	947	599	23	150
4	2278	784	499	23	126
4,5	1943	647	425	22	112
5	1657	523	353	21	96
5,5	1417	419	307	19	80
6	1190	340	238	18	68
6,5	1035	280	186	18	60
7	893	219	161	15	48
7,5	753	173	132	12	36
8	636	133	101	11	29
8,5	543	104	83	8	26
9	456	81	63	6	24
9,5	364	57	48	6	18
10	303	47	35	6	15

FIGURE 4

Tissue	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
Brain	329	131	75	3	24
Cancerous prostate	134	40	37	1	6
Cerebellum	17	8	1	0	6
Colon	21	11	4	0	0
Dystrophic muscle	41	18	8	0	1
Fetal brain	70	37	18	0	1
Fetal kidney	227	116	46	1	19
Fetal liver	13	7	2	0	0
Heart	30	15	7	0	1
Hypertrophic prostate	86	23	22	2	2
Kidney	10	7	3	0	0
Large intestine	21	8	4	0	1
Liver	23	9	6	0	0
Lung	24	12	4	0	1
Lung (cells)	57	38	6	0	4
Lymph ganglia	163	60	23	2	12
Lymphocytes	23	6	4	0	2
Muscle	33	16	6	0	4
Normal prostate	181	61	45	7	11
Ovary	90	57	12	1	2
Pancreas	48	11	6	0	1
Placenta	24	5	1	0	0
Prostate	34	16	4	0	2
Spleen	56	28	10	0	1
Substantia nigra	108	47	27	1	6
Suprenals	15	3	3	1	0
Testis	131	68	25	1	8
Thyroid	17	8	2	0	2
Umbilical cord	65	17	12	1	3
Uterus	28	15	3	0	2
Non tissue-specific	568	48	177	2	28
Total	2677	947	601	23	150

FIGURE 5



Plasmid name: pED6dpc2

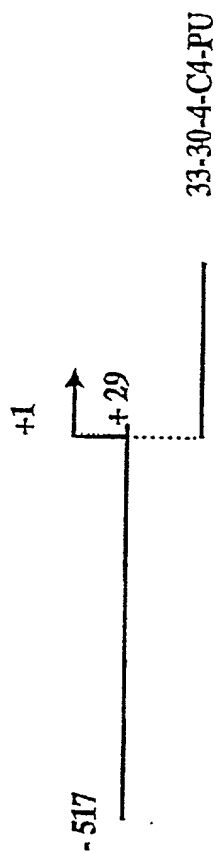
Plasmid size: 5374 bp

Comments/References: pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al.(1991), NAR 19: 4485-4490.

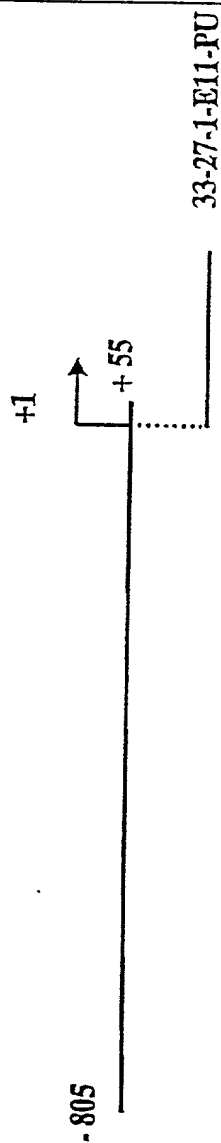
FIGURE 6

Description of Promoter structure isolated from SignalTag 5'ESTs

Promoter P13H2



Promoter P15B4



Promoter P29B6

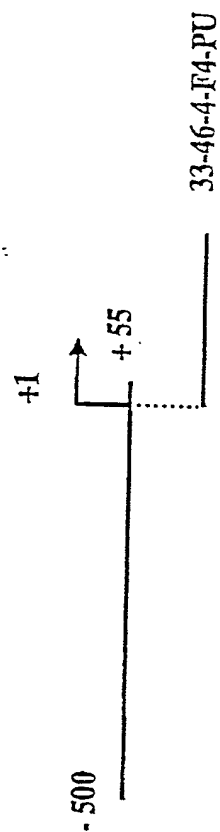


FIGURE 7

Description of Transcription Factor Binding Sites present on promoters isolated from SignalTag sequences.

Promoter sequence P13H2 (548 bp) :

Matrix	Position	Orientation	Score	Length	Sequence
CMYB_01	-502	+	0.983	9	TGTCAGTTG
MYOD_Q8	-501	-	0.981	10	CCCAACTGAC
S8_01	-444	-	0.960	11	AATAGAATTAG
S8_01	-425	+	0.968	11	AACTAAATTAG
DELTAEF1_01	-390	-	0.960	11	GCACACCTCAG
GATA_C	-364	-	0.964	11	AGATAAATCCA
CMYB_01	-349	+	0.958	9	CTTCAGTTG
GATA1_Q2	-343	+	0.959	14	TTGTAGATAGGACA
GATA_C	-339	+	0.953	11	AGATAGGACAT
TAL1ALPHA47_01	-235	+	0.973	16	CATAACAGATGGTAAG
TAL1BETA47_01	-235	+	0.983	16	CATAACAGATGGTAAG
TAL1BETAITF2_01	-235	+	0.978	16	CATAACAGATGGTAAG
MYOD_Q8	-232	-	0.954	10	ACCATCTGTT
GATA1_Q4	-217	-	0.953	13	TCAAGATAAAGTA
IK1_01	-126	+	0.963	13	AGTTGGGAATTCC
IK2_01	-126	+	0.985	12	AGTTGGGAATTCC
CREL_01	-123	+	0.982	10	TGGGAATTCC
GATA1_Q2	-98	+	0.950	14	TCAGTGATATGGCA
SRV_Q2	-41	-	0.951	12	TAAACAAAAACA
E2F_Q2	-33	+	0.957	8	TTTAGCGC
MZF1_Q1	-6	-	0.975	8	TGAGGGGA

Promoter sequence P16B4 (861 bp) :

Matrix	Position	Orientation	Score	Length	Sequence
NFY_Q8	-748	-	0.958	11	GGACCAATCAT
MZF1_Q1	-738	+	0.962	8	CCTGGGGA
CMYB_01	-684	+	0.984	9	TGACCGTTG
VMYB_Q2	-682	-	0.985	9	TCCAACGGT
STAT_01	-673	+	0.968	9	TTCTTGGA
STAT_01	-673	-	0.951	9	TTCCAGGA
MZF1_Q1	-556	-	0.956	8	TTGGGGGA
IK2_01	-451	+	0.965	12	GAATGGGAATTCC
MZF1_Q1	-424	+	0.988	8	AGAGGGGA
SRV_Q2	-368	-	0.955	12	GAAAAACAAAAACA
MZF1_Q1	-216	+	0.960	8	GAAGGGGA
MYOD_Q8	-190	+	0.981	10	AGCATCTGCC
DELTAEF1_01	-176	+	0.958	11	TCCACCTTCC
S8_01	6	-	0.992	11	GAGGCAATTAT
MZF1_Q1	16	-	0.988	8	AGAGGGGA

Promoter sequence P29B8 (555 bp) :

Matrix	Position	Orientation	Score	Length	Sequence
ARNT_01	-311	+	0.984	16	GGACTCACGTGCTGCT
NMYC_01	-309	+	0.985	12	ACTCACGTGCTG
USF_01	-309	+	0.985	12	ACTCACGTGCTG
USF_01	-309	-	0.985	12	OAGCAOGTGAGT
NMYC_01	-309	-	0.956	12	OAGCACGTGAGT
MYC MAX_02	-309	-	0.972	12	CAGCACGTGAGT
USF_C	-307	+	0.997	8	TCACGTGC
USF_C	-307	-	0.991	8	GCACGTGA
MZF1_Q1	-292	-	0.968	8	CATGGGGA
ELK1_Q2	-105	+	0.963	14	CTCTCCGGAAGCCT
OETB1P54_01	-102	+	0.974	10	TCCGGAAGCC
AP1_Q4	-42	-	0.963	11	AGTGACTGAAC
AP1FJ_Q2	-42	-	0.961	11	AGTGACTGAAC
PADS_C	45	+	1.000	9	TGTGGTCTC

Figure 8

98.2% identity in 113 aa overlap

```

      10      20      30      40      50      60
SeqID214 MVIRVYIASSSGSTAIAKKKQDVLGFLEANKIGFEEKDIAANEENRKWMRENVPENSRPA
          .....
AF042081 MVIRVYIASSSGSTAIAKKKQDVLGFLEANKIGFEEKDIAANEENRKWMRENVPENSRPA
      10      20      30      40      50      60

      70      80      90     100     110
SeqID214 TGNPLPPQIFNESQYRGDYDAFFEARENNAVYAFLGLTAPSGSKEAEVQAKQQ
          :: .....
AF042081 TGYPLPPQIFNESQYRGDYDAFFEARENNAVYAFLGLTAPPGSKEAEVQAKQQ
      70      80      90     100     110
```

FIGURE 9

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seqID215      MADDLKRFLYKKLPSVEGLHAIVSDRDGVPVIKVANDNAPEHALRPGFLSTFALATDQG
seqID185      MADDLKRFLYKKLPSVEGLHAIVSDRDGVPVVKVANDNAPEHALRPGFLSTFALATDQG
AF082526      MADDLKRFLYKKLPSVEGLHAIVSDRDGVPVIKVANDSAPEHALRPGFLSTFALATDQG
                *****
seqID215      SKLGLSKNKSIICYNTYQVVQFNRLPLVVSFIASSANTGLIVSLEKELAPLFEELRQV
seqID185      SKLGLSKNKSIICYNTYQVVQFNRLPLVVSFIASSANTGLIVSLEKELAPLFEELRQV
AF082526      SKLGLSKNKSIICYNTYQVVQFNRLPLVVSFIASSANTGLIVSLEKELAPLFEELIKV
                *****
seqID215      VEVS
seqID185      VEVS
AF082526      VEVS
                ****
```

FIGURE 10

91.3% identity in 230 aa overlap

```

      10      20      30      40      50      60
SeqID186 MASLGLQLVGYILGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSSKGLWMECATHSTG
          .....
AF072128 MASLGVQLVGYILGLLGLLGLTSLAMLLPNWRTSSYVGASIVTAVGFSSKGLWMECATHSTG
          10      20      30      40      50      60

      70      80      90     100     110     120
SeqID186 ITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVA
          .....
AF072128 ITQCDIYSTLLGLPADIQAAQAMMVTSSAMSSLACIISVVGMRCTVFCQDSRAKDRVAVV
          70      80      90     100     110     120

     130     140     150     160     170     180
SeqID186 GGVFFILGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLSLIAGII
          .....
AF072128 GGVFFILGGILGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLSLVAGVI
          130     140     150     160     170     180

     190     200     210     220     230
SeqID186 LCFSCSSQRNRSNYDAYQAQPLATRSSPRPGQPPKVSEFNSYSLTGYV
          .....
AF072128 LCFSCSPQGNRTNYYDGYQAQPLATRSSPRSAQPKAKSEFNSYSLTGYV
          190     200     210     220     230

```

FIGURE 11

98.3% identity in 121 aa overlap

```

                                10      20      30
seqID213      RFRKETDNAAIIMKVDKDRQMVVLEEEFRNISPEELKME
                .....
AB001993  MSDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKME
                10      20      30      40      50      60

                40      50      60      70      80      90
seqID213  LPERQPRFVVYSYKYVRDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV
                .....
AB001993  LPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV
                70      80      90      100     110     120

                100     110     120
seqID213  FEIRTTDDLTEAWLQEKL SFFR
                .....
AB001993  FEIRTTDDLTEAWLQEKL SFFR
                130     140
```

FIGURE 12

95.6% identity in 91 aa overlap

```

seq ID191                                10      20
                                         MGCVFQSTEDKCIFKIDWTLS
W36955      MFCPLKLILLPVLLDYSISGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS
              10      20      30      40      50      60

seq ID191      30      40      50      60      70      80
PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTyceIRL
W36955      PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDNLcNDGSLLLQDVQDVE
              70      80      90      100     110

seq ID191      90      100
KGEsQVFKKAVVLHVLPEEPKGTQMLT

```

FIGURE 13

99.0% identity in 381 aa overlap;

```

      10      20      30      40      50      60
seqID200  MLLSIGMLMLSATQVYTVLTVQLFAFLNPLPVEADILAYNFENASQTFDDLPARFGYRLP
          .....
AF037204  MLLSIGMLMLSATQVYTVLTVQLFAFLNLLPVEADILAYNFENASQTFDDLPARFGYRLP
      10      20      30      40      50      60

      70      80      90     100     110     120
id200    AEGLKGFLLNSKPENACEPIVPPPKDNSSGTFIVLIRRLDCNFDIKVLNAQRAGYKAAI
          .....
AF037204  AEGLKGFLLNSKPENACEPIVPPPKDNSSGTFIVLIRRLDCNFDIKVLNAQRAGYKAAI
      70      80      90     100     110     120

      130     140     150     160     170     180
id200    VHNVDSDDLISMGSNIDIEVLKKIDIPSVFIGESSASSLKDEFTYEKGGLILVPEFSLPL
          .....
AF037204  VHNVDSDDLISMGSNIDIEVLKKIDIPSVFIGESSANSLSLKDEFTYEKGGLILVPEFSLPL
      130     140     150     160     170     180

      190     200     210     220     230     240
id200    EYLIPLFLIIVGICLILIVIFMITKFVQDRHRARNRLRKDQLKKLPVHKFKKGDEYDVC
          .....
AF037204  EYLIPLFLIIVGICLILIVIFMITKFVQDRHRARNRLRKDQLKKLPVHKFKKGDEYDVC
      190     200     210     220     230     240

      250     260     270     280     290     300
id200    AICLDEYEDGDKLRILPCSHAYHCKCVDPWLTKTKKTCPVQKQKVVPSQGDSDSDTDSSQ
          .....
AF037204  AICLDEYEDGDKLRILPCSHAYHCKCVDPWLTKTKKTCPVQKQKVVPSQGDSDSDTDSSQ
      250     260     270     280     290     300

      310     320     330     340     350     360
id200    EENEVTEHTPLLRPLASVSAQSFGALSESRSHQNMTESDYEEDDNEDTDSSDAENEINE
          .....
AF037204  EENEVTEHTPLLRPLASVSAQSFGALSESRSHQNMTESDYEEDDNEDTDSSDAENEINE
      310     320     330     340     350     360

      370     380
id200    HDVVVQLQPNGERDYNIANTV
          .....
AF037204  HDVVVQLQPNGERDYNIANTV
      370     380

```

FIGURE 14

		10	20	30	40	50	60
seqID192		MSVFWGFGVLVPWFIPKGPNGR	VIITMLVTCSVCCYLFWL	IAIL	AQLNPLFGPQLKNET		
Y15286		MSVFWGFGVLVPWFIPKGPNGR	VIITMLVTCSVCCYLFWL	IAIL	AQLNPLFGPQLKNET		
		20	30	40	50	60	70
seqID192	IWYLKYHW						
	::::::						
Y15286	IWYLKYHW						
	80						

FIGURE 15

```

seqID201      -MDSRVS--SPEKQDKENFVGVNKRLGVCWILFSLFLLVIITFPISIWMLKIIREY
seqID227      -----MWLDP-----VFPLFPVG-----DH
X85116        MAEKRHTRDSEAQRLPDSFKDPSKGLGPCGWILVAFSFLFTVITFPISIWMCIKIKEY
               * .                ** .

seqID201      ERAVVFRIGRIQADKAGPGLILVLPCLDVFKVDLRTVTCNIPPQEILTRDSVTTQVDG
seqID227      Y-----LPHLHMDVLEG--LILVLPCLDVFKVDLRTVTCNIPPQEILTRDSVTTQVDG
X85116        ERAIIFRLGRILQGGAKGPGLFFILPCTDSFIKVD MRTISFDIPPQEILTKDSVTISVDG
               * . .      * * .*** * * .*** .*** .***** .*** ***

seqID201      VVYYRIYSAVSAVANVNDVHQATFLLAQTTLRNVLTQTLSQILAGREEIAHSIQTLTLLDD
seqID227      VVYYRIYSAVSAVANVNDVHQATFLLAQTTLRNVLTQTLSQILAGREEIAHSIQTLTLLDD
X85116        VVYYRVQNATLAVANITNADSATRLAQTTLRNVLTGTKNLSQILSDREEIAHNMQSTLDD
               ***** . * ***** . ** ***** .***** .***** .* .***

seqID201      ATELWGIRVARVEIKDVRIPVQLQRSMAAEAEATREARAKVLAEGEMSASKSLKSASMV
seqID227      ATELWGIRVARVEIKDVRIPVQLQRSMAAEAEATREARAKVLAEGEMNASKSLKSASMV
X85116        ATDAWGIKVERVEIKDVKL PVQLQRAMAAEAEASREARAKVIAAEGEMNASRALKEASMV
               ** .*** .* ***** .***** .***** .***** .***** .*** **

seqID201      LAESPIALQLRYLQTLSTVATEKNSTIVFPLPMNILEGIGGVSYDNHKKLPNKA
seqID227      LAESPIALQLRYLQTLSTVATEKNSTIVFPLPMNILEGIGGVSYDNHKKLPNKA
X85116        ITESPAALQLRYLQTLTTIAAEKNSTIVFPLPIDMLQGIIGAKHSHLG-----
               ..*** ***** .* .***** .* .*** *

```

FIGURE 16

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Edwards, et al.
Appl. No. : Unknown
Filed : Herewith
For : EXTENDED cDNAs FOR SECRETED PROTEINS
Group Art Unit : Unknown

SEQUENCE SUBMISSION

Assistant Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

A copy of the Sequence Listing in computer readable form as required by 37 C.F.R. § 1.821(e) is submitted herewith.

As required by 37 C.F.R. § 1.821(f), the data on the enclosed disk is identical to the Sequence Listing in the application filed herewith.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: Nov. 13, 1998

By: Daniel Hart
Daniel Hart
Registration No. 40,637
Attorney of Record
620 Newport Center Drive
Sixteenth Floor
Newport Beach, CA 92660
(619) 235-8550

SEQUENCE LISTING

<110> Edwards, Jean-Baptiste Dumas Milne
 Duclert, Aymeric
 Bougueleret, Lydie

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<213> Artificial Sequence

<220>
<221> Oligonucleotide

<400> 15
ccagcagagt cacgagagag actacacgg 29

<210> 16
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> Oligonucleotide

<400> 16
cacgagagag actacacggg actgg 25

<210> 17
<211> 526
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> complement(261..376)
<223> blastn

<221> misc_feature
<222> complement(380..486)
<223> blastn

<221> misc_feature
<222> complement(110..145)
<223> blastn

<221> misc_feature
 <222> complement(196..229)
 <223> blastn

<221> sig_peptide
 <222> 90..140
 <223> Von Heijne matrix

<400> 17
 aatatrarac agctacaata ttccagggcc artcacttgc cattttctcat aacagcgtca 60
 gagagaaaaga actgactgar acgtttgag atg aag aaa gtt ctc ctc ctg atc 113
 Met Lys Lys Val Leu Leu Leu Ile
 -15 -10
 aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag 161
 Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
 -5 1 5
 gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr 209
 Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
 10 15 20
 wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att 257
 Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
 25 30 35
 cca ttt cca aga ttt cca tgg ttt aga cgt aan ttt cct att cca ata 305
 Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
 40 45 50 55
 cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa 354
 Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
 60 65
 ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat 414
 caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta 474
 gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aa 526

<210> 18
 <211> 17
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> 1..17
 <223> Von Heijne matrix
 score 8.2
 seq LLLITAILAVAVG/FP

<400> 18
 Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
 1 5 10 15
 Gly

<210> 19
 <211> 822
 <212> DNA
 <213> Homo Sapiens

<220>

<221> misc_feature
 <222> 260..464
 <223> blastn

<221> misc_feature
 <222> 118..184
 <223> blastn

<221> misc_feature
 <222> 56..113
 <223> blastn

<221> misc_feature
 <222> 454..485
 <223> blastn

<221> misc_feature
 <222> 118..545
 <223> blastn

<221> misc_feature
 <222> 65..369
 <223> blastn

<221> misc_feature
 <222> 61..399
 <223> blastn

<221> misc_feature
 <222> 408..458
 <223> blastn

<221> misc_feature
 <222> 60..399
 <223> blastn

<221> misc_feature
 <222> 393..432
 <223> blastn

<221> sig_peptide
 <222> 346..408
 <223> Von Heijne matrix

<400> 19
 actcctttta gcataggggc ttcggcgcca gcggccagcg ctagtccgtc tggtaagtgc 60
 ctgatgccga gttccgtctc tcgcgtcttt tcctgggtccc aggcaaagcg gasgnagatc 120
 ctcaaacggc ctagtgtctc gcgcttccgg agaaaatcag cgggtctaatt aattcctctg 180
 gtttggtgaa gcagttacca agaattctca accctttccc acaaaagcta attgagtaca 240
 cgttcctgtt gagtacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg 300
 aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt 357
 Met Trp Trp Phe
 -20
 cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct 405
 Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
 -15 -10 -5
 gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata 453
 Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile

1	5	10	15	
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca raa				501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa				
	20	25	30	
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgt caa				549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln				
	35	40	45	
aaa tagaaatcag gaarataatt caacttaaag aakttcattt catgaccaa				602
Lys				
ctcttcaraa acatgtcttt acaagcatat ctcttgattt gctttctaca ctgttgaatt				662
gtctggcaat atttctgcag tggaaaattt gatttarmta gttcttgact gataaatatg				722
gtaaggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaw				782
tttgaaataa aatgatatga gagtgcacaa aaaaaaaaaa				822

<210> 20
 <211> 21
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> 1..21
 <223> Von Heijne matrix
 score 5.5
 seq SFLPSALVIWTS/AF

<400> 20
 Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
 1 5 10 15
 Ile Trp Thr Ser Ala
 20

<210> 21
 <211> 405
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> misc_feature
 <222> complement(103..398)
 <223> blastn

<221> sig_peptide
 <222> 185..295
 <223> Von Heijne matrix

<400> 21	
atcaccttct tctccatcct tctctgggcc agtccccarc ccagtccttc tctgacctg	60
cccagoccaa gtcagccttc agcacgcgct tttctgcaca cagatattcc aggcctacct	120
ggcattccag gacctccgma atgatgctcc agtcccttac aagcgcttcc tggatgaggg	180
tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg	229
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val	
-35 -30 -25	
aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc	277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala	
-20 -15 -10	

```

ctg tcc ccc tgt ctg acc gct cca aak tcc ccc cgg ctt gct atg atg      325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
   -5              1              5              10
cct gac aac taaatattcct tatccaaatc aataaarwra raatcctccc      374
Pro Asp Asn
tcgaraagg tttctaaaaa caaaaaaaaaa a      405

```

```

<210> 22
<211> 37
<212> PRT
<213> Homo Sapiens

```

```

<220>
<221> SIGNAL
<222> 1..37
<223> Von Heijne matrix
      score 5.9
      seq LSYASSALSPCLT/AP

```

```

<400> 22
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
1              5              10              15
Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
      20              25              30
Ser Pro Cys Leu Thr
      35

```

```

<210> 23
<211> 496
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> misc_feature
<222> 149..331
<223> blastn

```

```

<221> misc_feature
<222> 328..485
<223> blastn

```

```

<221> misc_feature
<222> complement(182..496)
<223> blastn

```

```

<221> sig_peptide
<222> 196..240
<223> Von Heijne matrix

```

```

<400> 23
aaaaaattgg tcccagtttt caccctgccg cagggctggc tggggagggc agcggtttag      60
attagccgtg gcctaggccg tttaacgggg tgacacgagc ntgcagggcc gagtccaagg      120
cccgagata ggaccaaccg tcaggaatgc gaggaatgtt tttcttcgga ctctatcgag      180
gcacacagac agacc atg ggg att ctg tct aca gtg aca gcc tta aca ttt      231
          Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
          -15              -10              -5

```

```

gcc ara gcc ctg gac ggc tgc aga aat ggc att gcc cac cct gca agt      279
Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
      1          5          10
gag aag cac aga ctc gag aaa tgt agg gaa ctc gag asc asc cac tcg      327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser
      15          20          25
gcc cca gga tca acc cas cac cga aga aaa aca acc aga aga aat tat      375
Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
      30          35          40          45
tct tca gcc tgaaatgaak ccgggatcaa atggttgctg atcaragccc      424
Ser Ser Ala
atattttaat tggaagagtc aaattgasca ttattaaata aagcttggtt aatatgtctc      484
aaacaaaaaa aa      496

```

```

<210> 24
<211> 15
<212> PRT
<213> Homo Sapiens

```

```

<220>
<221> SIGNAL
<222> 1..15
<223> Von Heijne matrix
      score 5.5
      seq ILSTVTALTFFAXA/LD

```

```

<400> 24
Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Xaa Ala
      1          5          10          15

```

```

<210> 25
<211> 623
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> sig_peptide
<222> 49..96
<223> Von Heijne matrix

```

```

<400> 25
aaagatccct gcagcccggc aggagagaag gctgagcctt ctggcgctc atg gag agg      57
                                   Met Glu Arg
                                   -15
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
      -10          -5          1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
      5          10          15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac      201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
      20          25          30          35
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta      249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
      40          45          50

```



```

cgc gtc ctg ctc agc aaa cgc tgt gct ccc aga tgt ccc aac gac aac      297
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
      55      60      65
atg aak ttc gaa tgg tcg ccg gcc ccc atg gtg caa ggc gtg atc acc      345
Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
      70      75      80
agg cgc tgc tgt tcc tgg gct ctc tgc aac agg gca ctg acc cca cag      393
Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
      85      90      95
gag ggg cgc tgg gcc ctg cra ggg ggg ctc ctg ctc cag gac cct tcg      441
Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser
      100      105      110      115
agg ggc ara aaa acc tgg gtg cgg cca cag ctg ggg ctc cca ctc tgc      489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
      120      125      130
ctt ccc awt tcc aac ccc ctc tgc cca rgg gaa acc cag gaa gga      534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
      135      140      145
taacactgtg ggtgccccca cctgtgcatt gggaccacra cttcaccctc ttggaracaa      594
taaactctca tgcccccaaa aaaaaaaaaa      623

```

```

<210> 26
<211> 16
<212> PRT
<213> Homo Sapiens

<220>
<221> SIGNAL
<222> 1..16
<223> Von Heijne matrix
      score 10.1
      seq LVLTLCTLPLAVA/SA

<400> 26
Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
1          5          10          15

```

```

<210> 27
<211> 848
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> sig_peptide
<222> 32..73
<223> Von Heijne matrix

```

```

<400> 27
aactttgcct tgtgttttcc accctgaaag a atg ttg tgg ctg ctc ttt ttt      52
                        Met Leu Trp Leu Leu Phe Phe
                        -10
ctg gtg act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat      100
Leu Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn
      -5          1          5
gct ttt aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca      148
Ala Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala

```

10	15	20	25	
tat gcc tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct				196
Tyr Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala				
	30	35	40	
ttc tcc atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat				244
Phe Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His				
	45	50	55	
gtc cta ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt				292
Val Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val				
	60	65	70	
aca gac cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca				340
Thr Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser				
	75	80	85	
gcc ata aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat				388
Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn				
	90	95	100	105
gac caa act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc				436
Asp Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro				
	110	115	120	
atg gac cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt				484
Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe				
	125	130	135	
tgc atc atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg				532
Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp				
	140	145	150	
caa cgt ada ara aag aac aaa gaa cca tct gaa gtg gat gac gct gaa				580
Gln Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu				
	155	160	165	
rat aak tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat				628
Xaa Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp				
	170	175	180	185
ccc ctg gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag				676
Pro Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu				
	190	195	200	
gat gag agg ctc acc cct ctc tgaagggtg ttgtttctgct tcttcaaraa				727
Asp Glu Arg Leu Thr Pro Leu				
	205			
attaaacatt tgtttctgtg tgactgctga gcacacctgaa ataccaagag cagatcatat				787
wttttgtttc accattcttc ttttgtaata aattttgaaat gtgcttgaaa aaaaaaaaaa				847
c				848

<210> 28

<211> 14

<212> PRT

<213> Homo Sapiens

<220>

<221> SIGNAL

<222> 1..14

<223> Von Heijne matrix

score 10.7

seq LWLLFFLVTAIHA/EL

<400> 28

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala

1

5

10

<210> 29
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> Oligonucleotide

<400> 29
gggaagatgg agatagtatt gcctg

25

<210> 30
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> Oligonucleotide

<400> 30
ctgccatgta catgatagag agattc

26

<210> 31
<211> 546
<212> DNA
<213> Homo Sapiens

<220>
<221> promoter
<222> 1..517

<221> transcription start site
<222> 518

<221> protein_bind
<222> 17..25
<223> matinspector prediction
name CMYB_01
score 0.983
sequence tgtcagttg

<221> protein_bind
<222> complement(18..27)
<223> matinspector prediction
name MYOD_Q6
score 0.961
sequence cccaactgac

<221> protein_bind
<222> complement(75..85)
<223> matinspector prediction
name S8_01
score 0.960
sequence aatagaattag

```

<221> protein_bind
<222> 94..104
<223> matinspector prediction
      name S8_01
      score 0.966
      sequence aactaaattag

<221> protein_bind
<222> complement(129..139)
<223> matinspector prediction
      name DELTAEF1_01
      score 0.960
      sequence gcacacctcag

<221> protein_bind
<222> complement(155..165)
<223> matinspector prediction
      name GATA_C
      score 0.964
      sequence agataaatcca

<221> protein_bind
<222> 170..178
<223> matinspector prediction
      name CMYB_01
      score 0.958
      sequence cttcagttg

<221> protein_bind
<222> 176..189
<223> matinspector prediction
      name GATA1_02
      score 0.959
      sequence ttgtagataggaca

<221> protein_bind
<222> 180..190
<223> matinspector prediction
      name GATA_C
      score 0.953
      sequence agataggacat

<221> protein_bind
<222> 284..299
<223> matinspector prediction
      name TAL1ALPHA47_01
      score 0.973
      sequence cataacagatggtaag

<221> protein_bind
<222> 284..299
<223> matinspector prediction
      name TAL1BETA47_01
      score 0.983
      sequence cataacagatggtaag

<221> protein_bind
<222> 284..299

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<223> matinspector prediction
name TAL1BETAITF2_01
score 0.978
sequence cataacagatggtaag

<221> protein_bind
<222> complement(287..296)
<223> matinspector prediction
name MYOD_Q6
score 0.954
sequence accatctgtt

<221> protein_bind
<222> complement(302..314)
<223> matinspector prediction
name GATA1_04
score 0.953
sequence tcaagataaaagta

<221> protein_bind
<222> 393..405
<223> matinspector prediction
name IK1_01
score 0.963
sequence agttgggaattcc

<221> protein_bind
<222> 393..404
<223> matinspector prediction
name IK2_01
score 0.985
sequence agttgggaattc

<221> protein_bind
<222> 396..405
<223> matinspector prediction
name CREL_01
score 0.962
sequence tgggaattcc

<221> protein_bind
<222> 423..436
<223> matinspector prediction
name GATA1_02
score 0.950
sequence tcagtgatatggca

<221> protein_bind
<222> complement(478..489)
<223> matinspector prediction
name SRY_02
score 0.951
sequence taaaacaaaaca

<221> protein_bind
<222> 486..493
<223> matinspector prediction
name E2F_02

score 0.957
sequence tttagcgc

<221> protein_bind
<222> complement(514..521)
<223> matinspector prediction
name MZF1_01
score 0.975
sequence tgagggga

<400> 31
tgagtgcagt gttacatgtc agttgggtta agtttggtta tgtcattcaa atcttctatg 60
tcttgatttg cctgctaatt ctattatttc tggaactaaa ttagtttgat ggttctatta 120
gttattgact gaggtgtgct aatctcccat tatgtggatt tatctatttc ttcagttgta 180
gataggacat tgatagatac ataagtacca ggacaaaagc agggagatct tttttccaaa 240
atcaggagaa aaaaatgaca tctggaaaac ctatagggaa aggcataaca gatggtaagg 300
atactttatc ttgagtagga gagccttcct gtggcaacgt ggagaaggga agaggtcgta 360
gaattgagga gtcagctcag ttagaagcag ggagttggga attccgttca tgtgatttag 420
catcagtgat atggcaaata tgggactaag ggtagtgatc agagggttaa aattgtgtgt 480
tttgttttag cgctgctggg gcatcgcctt gggtcccctc aaacagattc ccatgaatct 540
cttcat 546

<210> 32
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> Oligonucleotide

<400> 32
gtaccagggga ctgtgacat tgc 23

<210> 33
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Oligonucleotide

<400> 33
ctgtgacat tgctcccaag agag 24

<210> 34
<211> 861
<212> DNA
<213> Homo Sapiens

<220>
<221> promoter
<222> 1..806

<221> transcription start site
<222> 807

<221> protein_bind
 <222> complement(60..70)
 <223> matinspector prediction
 name NFY_Q6
 score 0.956
 sequence ggaccaatcat

<221> protein_bind
 <222> 70..77
 <223> matinspector prediction
 name MZF1_01
 score 0.962
 sequence cctgggga

<221> protein_bind
 <222> 124..132
 <223> matinspector prediction
 name CMYB_01
 score 0.994
 sequence tgaccgttg

<221> protein_bind
 <222> complement(126..134)
 <223> matinspector prediction
 name VMYB_02
 score 0.985
 sequence tccaacggt

<221> protein_bind
 <222> 135..143
 <223> matinspector prediction
 name STAT_01
 score 0.968
 sequence ttcctggaa

<221> protein_bind
 <222> complement(135..143)
 <223> matinspector prediction
 name STAT_01
 score 0.951
 sequence ttccaggaa

<221> protein_bind
 <222> complement(252..259)
 <223> matinspector prediction
 name MZF1_01
 score 0.956
 sequence ttggggga

<221> protein_bind
 <222> 357..368
 <223> matinspector prediction
 name IK2_01
 score 0.965
 sequence gaatgggatttc

<221> protein_bind
 <222> 384..391

<223> matinspector prediction
 name MZF1_01
 score 0.986
 sequence agagggga

<221> protein_bind
 <222> complement(410..421)
 <223> matinspector prediction
 name SRY_02
 score 0.955
 sequence gaaaacaaaaca

<221> protein_bind
 <222> 592..599
 <223> matinspector prediction
 name MZF1_01
 score 0.960
 sequence gaagggga

<221> protein_bind
 <222> 618..627
 <223> matinspector prediction
 name MYOD_Q6
 score 0.981
 sequence agcatctgcc

<221> protein_bind
 <222> 632..642
 <223> matinspector prediction
 name DELTAEF1_01
 score 0.958
 sequence tcccaccttc

<221> protein_bind
 <222> complement(813..823)
 <223> matinspector prediction
 name S8_01
 score 0.992
 sequence gaggcaattat

<221> protein_bind
 <222> complement(824..831)
 <223> matinspector prediction
 name MZF1_01
 score 0.986
 sequence agagggga

<400> 34

tactataggg	cacgcgtggt	cgacggccgg	gctgttctg	agcagagggc	atgtcagtaa	60
tgattgggtcc	ctggggaagg	tctggctggc	tccagcacag	tgaggcattt	aggtatctct	120
cggtgaccgt	tggattcctg	gaagcagtag	ctgttctggt	tggatctggt	agggacaggg	180
ctcagagggc	taggcacgag	ggaaggctcag	aggagaaggs	aggsarggcc	cagtgagarg	240
ggagcatgcc	ttcccccaac	cctggcttsc	ycttggyam	agggcgkty	tgggmacttr	300
aaytcagggc	ccaascagaa	scacaggccc	aktcntggct	smaagcacia	tagcctgaat	360
gggatttcag	gttagncagg	gtgagagggg	aggctctctg	gcttagtttt	gttttgtttt	420
ccaaatcaag	gtaacttgct	cccttctgct	acgggccttg	gtcttggtt	gtcctcacc	480
agtcggaact	ccctaccact	ttcaggagag	tggttttagg	cccgtggggc	tggtctgttc	540
caagcagtgt	gagaacatgg	ctggtagagg	ctctagctgt	gtgcggggcc	tgaaggggag	600

tggtgtctcg	cccaaagagc	atctgccc	at	ttccacctt	cccttctccc	accagaagct	660
tgcttgagct	gtttggacaa	aaatccaaac	cccacttggc	tactctggcc	tggttcagc		720
ttggaaccca	atacctaggc	ttacaggcca	tcctgagcca	ggggcctctg	gaaattctct		780
tcctgatggg	cctttagggt	tgggcacaaa	atataattgc	ctctcccctc	tccattttc		840
tctcttgga	gcaatggtca	c					861

<210> 35
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<220>
 <221> Oligonucleotide

<400> 35	
ctgggatgga aggcacgga	20

<210> 36
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<220>
 <221> Oligonucleotide

<400> 36	
gagaccacac agctagacaa	20

<210> 37
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 <213> Homo Sapiens

<220>
 <221> promoter
 <222> 1..500

<221> transcription start site
 <222> 501

<221> protein_bind
 <222> 191..206
 <223> matinspector prediction
 name ARNT_01
 score 0.964
 sequence ggactcacgtgctgct

<221> protein_bind
 <222> 193..204
 <223> matinspector prediction
 name NMYC_01
 score 0.965
 sequence actcacgtgctg

<221> protein_bind

<222> 193..204
 <223> matinspector prediction
 name USF_01
 score 0.985
 sequence actcacgtgctg

<221> protein_bind
 <222> complement(193..204)
 <223> matinspector prediction
 name USF_01
 score 0.985
 sequence cagcacgtgagt

<221> protein_bind
 <222> complement(193..204)
 <223> matinspector prediction
 name NMYC_01
 score 0.956
 sequence cagcacgtgagt

<221> protein_bind
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 <223> matinspector prediction
 name MYCMAX_02
 score 0.972
 sequence cagcacgtgagt

<221> protein_bind
 <222> 195..202
 <223> matinspector prediction
 name USF_C
 score 0.997
 sequence tcacgtgc

<221> protein_bind
 <222> complement(195..202)
 <223> matinspector prediction
 name USF_C
 score 0.991
 sequence gcacgtga

<221> protein_bind
 <222> complement(210..217)
 <223> matinspector prediction
 name MZF1_01
 score 0.968
 sequence catgggga

<221> protein_bind
 <222> 397..410
 <223> matinspector prediction
 name ELK1_02
 score 0.963
 sequence ctctccggaagcct

<221> protein_bind
 <222> 400..409
 <223> matinspector prediction

name CETS1P54_01
score 0.974
sequence tccggaagcc

<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
name AP1_Q4
score 0.963
sequence agtgactgaac

<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
name AP1FJ_Q2
score 0.961
sequence agtgactgaac

<221> protein_bind
<222> 547..555
<223> matinspector prediction
name PADS_C
score 1.000
sequence tgtggtctc

<400> 37

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kawaagctca	gcaccggtgc	ccatcacagg	gccggcagca	cacacatccc	attactcaga	180
aggaactgac	ggactcacgt	gctgctccgt	ccccatgagc	tcagtggacc	tgtctatgta	240
gagcagtcag	acagtgcctg	ggatagagtg	agagttcagc	cagtaaattcc	aagtgattgt	300
catttcctgtc	tgcattagta	actcccaacc	tagatgtgaa	aacttagttc	tttctcatag	360
gttgctctgc	ccatgggtccc	actgcagacc	caggcactct	ccggaagcct	ggaaatcacc	420
cgtgtcttct	gcctgctccc	gtcacatcc	cacacttggtg	ttcagtcact	gagttacaga	480
ttttgctctc	tcaattttctc	ttgtcttagt	cccatcctct	gttcccctgg	ccagtttgtc	540
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<210> 38

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<221> Oligonucleotide

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<210> 39

<211> 19

<212> DNA

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19

<210> 40
<211> 1098
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<221> polyA_site
<222> 1087..1098

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<223> homology
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est

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<221> misc_feature
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<223> homology
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
<222> 567..687
<223> homology
id :T34150
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<221> misc_feature
<222> 686..730
<223> homology
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<221> misc_feature
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<221> misc_feature
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<223> homology
id :N32314

est

<221> misc_feature
<222> 352..523
<223> homology
id :T77966
est

<221> misc_feature
<222> 218..351
<223> homology
id :T77966
est

<221> misc_feature
<222> 510..553
<223> homology
id :T77966
est

<221> misc_feature
<222> 550..917
<223> homology
id :AA464128
est

<400> 40

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ggctaaggac ggcagctcct ttagcggcag agttttccga gtgaccttct tg atg ctg      178
                                         Met Leu
gct gtt tct ctc acc gtt ccc ctg ctt gga gcc atg atg ctg ctg gaa      226
Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu Leu Glu
-10 -5 1 5
tct cct ata gat cca cag cct ctc agc ttc aaa gaa ccc ccg ctc ttg      274
Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro Leu Leu
10 15 20
ctt ggt gtt ctg cat cca aat acg aag ctg cga cag gca gaa agg ctg      322
Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu Arg Leu
25 30 35
ttt gaa aat caa ctt gtt gga ccg gag tcc ata gca cat att ggg gat      370
Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile Gly Asp
40 45 50
gtg atg ttt act ggg aca gca gat ggc cgg gtc gta aaa ctt gaa aat      418
Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu Glu Asn
55 60 65
ggt gaa ata gag acc att gcc ccg ttt ggt tcg ggc cct tgc aaa acc      466
Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys Lys Thr
70 75 80 85
cga ggt gat gag cct gtg tgt ggg aga ccc ctg ggt atc cgt ggc agg      514
Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg Gly Arg
90 95 100
gcc caa tgg gac tct ctt tgt ggc cga tgc ata caa agg gac tat ttg      562
Ala Gln Trp Asp Ser Leu Cys Gly Arg Cys Ile Gln Arg Asp Tyr Leu
105 110 115
aag taaatccctg gaaacgtgaa gtgaaactgc tgctgtcctc cgagacaccc      615
Lys
attgagggga agaacatgtc ctttgtgaat gatcttacag tcaactcagga tgggaggaag      675
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cagagaagaa catttaaagg gttaatatatt ttgaaacgtt ttcagataat atctatttga	785
ttattgtggc ttctatttga aatgtgtcta aaataaaatg ctgtttattt aaaatgaaaa	845
aaaaaaaaaa	855

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 <211> 1176
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 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 174..266
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<221> polyA_signal
 <222> 1144..1149

<221> polyA_site
 <222> 1165..1176

<221> misc_feature
 <222> 886..1134
 <223> homology
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<221> misc_feature
 <222> 756..894
 <223> homology
 id :AA595193
 est

<221> misc_feature
 <222> 655..755
 <223> homology
 id :AA595193
 est

<221> misc_feature
 <222> 167..367
 <223> homology
 id :W81213
 est

<221> misc_feature
 <222> 66..172
 <223> homology
 id :W81213
 est

<221> misc_feature
 <222> 429..508
 <223> homology
 id :W81213
 est

<221> misc_feature
<222> 756..894
<223> homology
id :AA150887
est

<221> misc_feature
<222> 536..643
<223> homology
id :AA150887
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<221> misc_feature
<222> 655..755
<223> homology
id :AA150887
est

<221> misc_feature
<222> 429..643
<223> homology
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<221> misc_feature
<222> 655..755
<223> homology
id :AA493644
est

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<222> 429..643
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<221> misc_feature
<222> 655..755
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<221> misc_feature
<222> 500..643
<223> homology
id :AA179182
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<221> misc_feature
<222> 655..755
<223> homology
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<221> misc_feature
<222> 756..847
<223> homology

id :AA179182
est

<221> misc_feature
<222> 3..338
<223> homology
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<221> misc_feature
<222> 334..374
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id :HUM524F05B
est

<221> misc_feature
<222> 886..1134
<223> homology
id :AA398156
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<221> misc_feature
<222> 756..894
<223> homology
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est

<400> 42

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tggccgctgg actccgctgc ctcccccatc tccccgccat ctgcgcccgagg agg atg      176
                                     Met
agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc tcc      224
Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Ser
-30                               -25                               -20                               -15
ttc tgg agc cct ttg tcc acc agg tcg ggg ggc act cat gcg tgc tcc      272
Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys Ser
-10                               -5                               1
gct tca atg aga caa ccc tgg gca agc ccc tgg tcc caa ggg aac atc      320
Ala Ser Met Arg Gln Pro Trp Ala Ser Pro Trp Ser Gln Gly Asn Ile
5                               10                               15
agt tct acg aga ccc tcc ctg ctg aga tgc gca aat tct ctc ccc agt      368
Ser Ser Thr Arg Pro Ser Leu Leu Arg Cys Ala Asn Ser Leu Pro Ser
20                               25                               30
aca aag gac aaa gcc aaa ggc ccc ttg tta gct ggc cat ccc tgc ccc      416
Thr Lys Asp Lys Ala Lys Gly Pro Leu Leu Ala Gly His Pro Cys Pro
35                               40                               45                               50
att ttt tcc cct ggt cct ttc ccc tgt ggc cac agg gaa gtg tgg cct      464
Ile Phe Ser Pro Gly Pro Phe Pro Cys Gly His Arg Glu Val Trp Pro
55                               60                               65
gaa tac ccc acc ccg gct cct ctg cac cca gag ctg ggg gcc acc tca      512
Glu Tyr Pro Thr Pro Ala Pro Leu His Pro Glu Leu Gly Ala Thr Ser
70                               75                               80
gaa gtg tca tct ctc tct gag cac gsa ttc ccc tgc agc agt cga gga      560
Glu Val Ser Ser Leu Ser Glu His Xaa Phe Pro Cys Ser Ser Arg Gly
85                               90                               95
ctg agc aga ttg agt gat gct ggg gca gan adg cct gag ang aaa ggt      608
Leu Ser Arg Leu Ser Asp Ala Gly Ala Xaa Xaa Pro Glu Xaa Lys Gly
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100	105	110	
gtt cag cca gtc gtt tgt aag gcg ctc gkc ggm act gct gaa acg ccc			656
Val Gln Pro Val Val Cys Lys Ala Leu Xaa Gly Thr Ala Glu Thr Pro			
115	120	125	130
cca ccc tgacagcccc atcctcaaag actgtcttaa ttactcatgg caggttctag			712
Pro Pro			
agacttaagg ggaaaagctg ctttcaaggc caccacatgt ctggtgctcc ccmaccagst			772
statctgcct wgtgttcatt ttgytatttt gtgasgtgag acagcaaaga ccaataaaaa			832
catattttat aagaacaaaa ggcytgggtg cctaccgkg tgggggcacw gtgggaagcc			892
ttctgmtagg gtgtcttgtg ctgtrtgggt tgttttgttt gccccyttat tttgctttgc			952
ttaccagtc ttcccytamt yttgatgst tyttaaccct caggcaaacc tgtgttcccc			1012
ctgtattcag gstytgcttt aaagcaagcc atgaggtgtg tggagtttct gtttagggca			1072
ttaaaaattc ccgcaaacta taaagagcaa tgttttcagt yttttaggat tagaagaatt			1132
acataaaaat taataaacat tttcaatgat ggaaaaaaaa aaaa			1176

<210> 43
 <211> 648
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 460..555
 <223> Von Heijne matrix
 score 4
 seq FSFMLLGMGGLP/GF

<221> polyA_signal
 <222> 614..619

<221> polyA_site
 <222> 635..648

<400> 43	
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tccttagagt tctccctcca ttagtagttg tcttagggtc tgtttctggg gagccctgcc	120
taagactcat gctacaagaa gttaaataag tttccogaag tcacacagct agcctctcat	180
cccttttcta ctgagaggaa gtggaatgca ctccgacaag gataaggttt tattgtgagc	240
tggccttgga attaaaccac caccaacaca cttttggatt atcagaaggt ggaaggagtg	300
caaatgccag ttacgggtgat gcgttcaaca tccttatctc cagtctttat gacgcctttc	360
ctgaatcaca ggtgcattgg ggtgcttcct cctccccagg actcccaccc aactttgtga	420
acacaacca cttagaggag ttatctcagc acattatga atg ttg ggg acc acg	474
Met Leu Gly Thr Thr	
-30	

ggc ctc ggg aca cag ggt cct tcc cag cag gct ctg ggc ttt ttc tcc	522
Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala Leu Gly Phe Phe Ser	
-25 -20 -15	
ttt atg tta ctt gga atg ggc ggg tgc ctg cct gga ttc ctg cta cag	570
Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro Gly Phe Leu Leu Gln	
-10 -5 1 5	
cct ccc aat cga tct cct act ttg cct gca tcc acc ttt gcc cat	615
Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser Thr Phe Ala His	
10 15 20	
taaagtcaat tctccacca taaaaaaaaaaa aaa	648

<210> 44

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<211> 1251
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 79..369
<223> Von Heijne matrix
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<221> polyA_signal
<222> 1217..1222

<221> polyA_site
<222> 1240..1251

<221> misc_feature
<222> 2..423
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<222> 463..520
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<221> misc_feature
<222> 418..467
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<221> misc_feature
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<223> homology
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<221> misc_feature
<222> 629..684
<223> homology
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<221> misc_feature
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<223> homology
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<221> misc_feature
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<221> misc_feature
<222> 14..343
<223> homology
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<221> misc_feature
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<221> misc_feature
<222> 463..494
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
<222> 1208..1237
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<222> 518..636
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<221> misc_feature
<222> 833..1195
<223> homology
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est

<400> 44

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gagaga	agggg	ggttc	atc	atg	gcg	gat	gac	cta	aag	cga	ttc	111
				Met	Ala	Asp	Asp	Leu	Lys	Arg	Phe	
aag	tta	cca	agt	gtt	gaa	ggg	ctc	cat	gcc	att	gtt	159
Lys	Leu	Pro	Ser	Val	Glu	Gly	Leu	His	Ala	Ile	Val	
gat	gga	gta	cct	gtt	att	aaa	gtg	gca	aat	gac	aat	207
Asp	Gly	Val	Pro	Val	Ile	Lys	Val	Ala	Asn	Asp	Asn	
gct	ttg	cga	cct	ggg	ttc	tta	tcc	act	ttt	gcc	ctt	255
Ala	Leu	Arg	Pro	Gly	Phe	Leu	Ser	Thr	Phe	Ala	Leu	
gga	agc	aaa	ctt	gga	ctt	tcc	aaa	aat	aaa	agt	atc	303
Gly	Ser	Lys	Leu	Gly	Leu	Ser	Lys	Asn	Lys	Ser	Ile	
aac	acc	tac	cag	gtg	gtt	caa	ttt	aat	cgt	tta	cct	351
Asn	Thr	Tyr	Gln	Val	Val	Gln	Phe	Asn	Arg	Leu	Pro	
ttc	ata	gcc	agc	agc	agt	gcc	aat	aca	gga	cta	att	399
Phe	Ile	Ala	Ser	Ser	Ser	Ala	Asn	Thr	Gly	Leu	Ile	
aag	gag	ctt	gct	cca	ttg	ttt	gaa	gaa	ctg	aga	caa	447
Lys	Glu	Leu	Ala	Pro	Leu	Phe	Glu	Glu	Leu	Arg	Gln	
tct	taat	ctgaca	gtg	ggtt	tcag	tgt	gtac	ctt	atct	tcatta	taaca	500
Ser												
atat	caat	ccc	agca	atctt	agact	acaat	aat	gctt	tta	tccat	gtgct	560
cccc	cttt	ttc	caact	tatac	taa	aga	acta	gcat	atagat	gta	atata	620
ttg	ctat	att	ttct	ggtg	ta	aggt	cttt	ct	tatt	tagtga	gat	680
atg	gttc	agt	ctat	cacagc	tccc	atgg	ag	ttag	tctgg	cacc	agatat	740
ttct	attc	ag	tgg	attag	aa	actgg	t	acatt	gatcc	act	tgagccg	800
cca	attg	tac	aat	atg	ccca	ggct	tg	caga	ataa	agccaa	ctttt	860
taag	gac	ata	tttt	ctt	tca	gatt	at	gttt	tatt	ctttg	catt	920
atg	gct	tggt	aaa	agta	ata	aat	cagt	ac	aat	caact	aat	980
ttg	cagt	ata	gat	ga	atatt	act	aat	cagt	ttg	att	ctt	1040

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gtgttttaaat gtttgtgtgt tcttcataaa atttaaatac aattcgttat tctgtttcca 1160
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aaatagtatt tttaaaagta aaaaaaaaaa a 1251

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<210> 45
<211> 1524
<212> DNA
<213> Homo sapiens

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<220>
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<221> polyA_signal
<222> 1510..1515

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<221> polyA_site
<222> 1506..1519

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<221> misc_feature
<222> 1048..1504
<223> homology
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<221> misc_feature
<222> 597..846
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      est

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<223> homology
      id :T86158

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est

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id :AA116709
est

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actctgaaat gassgattag aggtgttcaa ggragcaaag agcttcagcc tgaagacaag      120
ggagcagtcct ctgaagacgc ttctactgag aggtctgcc atg gcc tct ctt ggc      174
                               Met Ala Ser Leu Gly
                               -20
ctc caa ctt gtg ggc tac atc cta ggc ctt ctg ggg ctt ttg ggc aca      222
Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu Gly Leu Leu Gly Thr
                               -15                               -10                               -5
ctg gtt gcc atg ctg ctc ccc agc tgg aaa aca agt tct tat gtc ggt      270
Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr Ser Ser Tyr Val Gly
                               1                               5                               10
gcc agc att gtg aca gca gtt ggc ttc tcc aag ggc ctc tgg atg gaa      318
Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu Trp Met Glu
                               15                               20                               25
tgt gcc aca cac agc aca ggc atc acc cag tgt gac atc tat agc acc      366
Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys Asp Ile Tyr Ser Thr
                               30                               35                               40                               45
ctt ctg ggc ctg ccc gct gac atc cak gct gcc cag gcc atg atg gtg      414
Leu Leu Gly Leu Pro Ala Asp Ile Xaa Ala Ala Gln Ala Met Met Val
                               50                               55                               60
aca tcc agt gca atc tcc tcc ctg gcc tgc att atc tct gtg gtg ggc      462
Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly
                               65                               70                               75
atg ara tgc aca gtc ttc tgc cag gaa tcc cga gcc aaa gac aga gtg      510
Met Xaa Cys Thr Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val
                               80                               85                               90
gcg gta gca ggt gga gtc ttt ttc atc ctt gga ggc ctc ctg gga ttc      558
Ala Val Ala Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe
                               95                               100                               105
att cct gtt gcc tgg aat ctt cat ggg atc cta cgg gac ttc tac tca      606
Ile Pro Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser
                               110                               115                               120                               125
cca ctg gtg cct gac agc atg aaa ttt gag att gga gag gct ctt tac      654
Pro Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr
                               130                               135                               140
ttg ggc att att tct tcc ctg ttc tcc ctg ata gct gga atc atc ctc      702
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile Leu
                               145                               150                               155
tgc ttt tcc tgc tca tcc cag aga aat cgc tcc aac tac tac gat gcc      750
Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr Asp Ala
                               160                               165                               170
tac caa gcc caa cct ctt gcc aca agg agc tct cca agg cct ggt caa      798
Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg Pro Gly Gln
                               175                               180                               185
cct ccc aaa gtc aag agt gag ttc aat tcc tac agc ctg aca ggg tat      846
Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser Leu Thr Gly Tyr
                               190                               195                               200                               205
gtg tgaagaacca ggggccagag ctgggggggtg gctgggtctg tgaaaaacag      899
Val
```


tggacagcac	cccgagggcc	acaggtgagg	gacactacca	ctggatcgtg	tcagaaggtg	959
ctgctgaggg	tagactgact	ttggccattg	gattgagcaa	aggcagaaat	gggggctagt	1019
gtaacagcat	gcaggttgaa	ttgccaagga	tgctcgccat	gccagccttt	ctgttttcct	1079
caccttgctg	ctcccctgcc	ctaagtcccc	aaccctcaac	ttgaaacccc	attcccttaa	1139
gccaggamtc	agaggatccc	tytgccctck	ggtttamctg	ggactccatc	cccaaaccga	1199
ctaatacat	cccactgact	gaccctctgt	gatcaaagac	cctccctctg	gctgagggtg	1259
gstyttagct	cattgctggg	gatgggaagg	agaagcagtg	gctttystgg	gcattgctyt	1319
aacctamtty	tcaagcttcc	ctccaaagaa	amtgattggc	cctggaacct	ccatcccact	1379
yttgttatga	ctccacagtg	tccagamtaa	tttgtgcatg	aactgaaata	aaaccatcct	1439
acggtatyca	gggaacagaa	agcaggatgc	aggatgggag	gacaggaagg	cagcctggga	1499
catttaaaaa	aataaaaaaa	aaaaa				1524

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<221> polyA_site
 <222> 598..610

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<221> misc_feature
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 est

<221> misc_feature
 <222> 423..520
 <223> homology
 id :AA531561
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<221> misc_feature
 <222> 518..564
 <223> homology
 id :AA531561
 est

<221> misc_feature
 <222> 276..313
 <223> homology

id :AA531561
est

<221> misc_feature
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 est

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 est

<221> misc_feature
 <222> 276..313
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 est

<221> misc_feature
 <222> 125..262
 <223> homology
 id :W47031
 est

<400> 46

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gcgctag	gcc cgctt	ggagt	tctgag	ccga	tggaag	agatt	cactc	atg	ttt	gca	ccc	117
										Met	Phe	
										Ala	Pro	
										-30		
gcg	gtg	atg	cgt	gct	ttt	cgc	aag	aac	aag	act	ctc	165
Ala	Val	Met	Arg	Ala	Phe	Arg	Lys	Asn	Lys	Thr	Leu	
			-25				-20			-15		
ccc	atg	ttg	ttg	ctg	att	gtt	gga	ggt	tct	ttt	ggt	213
Pro	Met	Leu	Leu	Leu	Ile	Val	Gly	Gly	Ser	Phe	Gly	
		-10				-5			1			
tct	caa	atc	cga	tat	gat	gct	gtg	aag	agt	aaa	atg	261
Ser	Gln	Ile	Arg	Tyr	Asp	Ala	Val	Lys	Ser	Lys	Met	
5			10				15			20		
gaa	aaa	aaa	ccg	aaa	gag	aat	aaa	ata	tct	tta	gag	309
Glu	Lys	Lys	Pro	Lys	Glu	Asn	Lys	Ile	Ser	Leu	Glu	
			25			30			35			
gga	agt	atc	tgt	tgaagg	gcta	ctatct	tttcc	ttggc	ccttc	tccctt	gttg	361
Gly	Ser	Ile	Cys									
			40									
ggact	caatc	tccag	actat	ctcccc	agag	aatctt	gtca	aggctt	ggct	ttaag	ctttg	421
ttggg	aaaat	caaag	actcc	aagttt	gatg	actgga	agaa	tattcg	agga	cccagg	cctt	481
gggaag	atcc	tgacct	cctc	caagga	agaa	atccagg	aaaa	gcctta	agac	taagaca	act	541

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tgactctgct gattcttttt tccttttttt ttttaaataa aaatactatt aactggaaaa    601
aaaaaaaaaa                                                                610

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<212> DNA
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<221> polyA_signal
<222> 1334..1339

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<221> polyA_site
<222> 1357..1370

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<221> misc_feature
<222> 113..420
<223> homology
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      est

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<221> misc_feature
<222> 406..482
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<223> homology
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<223> homology
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<223> homology
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<223> homology
id :R74123
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<221> misc_feature
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<221> misc_feature
<222> 406..646
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<221> misc_feature
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<221> misc_feature
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id :C06030
est

<221> misc_feature
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est

<221> misc_feature
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est

<221> misc_feature
<222> 1080..1177
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id :N54909

est

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est

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<221> misc_feature
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<400> 47

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cctgtttccac	caagtgaag	aaggtactta	ctcttgtagc	tcctgttcag	ccagggtgcat	180
taacagacct	ccctacagct	gtaggaacta	ctgtcccaga	gctgaggcaa	ggggatttct	240
caggtcattt	ggagaacaag	tgcttttagta	gtagtttaaa	gtagtaactg	ctactgtatt	300
tagtgggggtg	gaattcagaa	gaaatttgaa	gaccagatca	tgggtggtct	gcatgtga	358
atg aac ach	ttt gag cca	gac agc ctg	gct gtc att	gct ttc ttc	ctc	406
Met Asn Thr	Phe Glu Pro	Asp Ser Leu	Ala Val Ile	Ala Phe Phe	Leu	
-35		-30		-25		
ccc att tgg	acc ttc tct	gcc ctt aca	ttt ttg ttt	ctc cat cta	cca	454
Pro Ile Trp	Thr Phe Ser	Ala Leu Thr	Phe Leu Phe	Leu His Leu	Pro	
-20		-15		-10	-5	
cca tcc acc	agt cta ttt	att aac tta	gca aga gga	caa ata aag	ggc	502
Pro Ser Thr	Ser Leu Phe	Ile Asn Leu	Ala Arg Gly	Gln Ile Lys	Gly	
	1	5		10		
cct ctt ggc	ttg att ttg	ctt ctt tct	ttc tgt gga	gga tat act	aag	550
Pro Leu Gly	Leu Ile Leu	Leu Leu Ser	Phe Cys Gly	Gly Tyr Thr	Lys	
	15	20		25		
tgc gac ttt	gcc cta tcc	tat ttg gaa	atc cct aac	aga att gag	ttt	598
Cys Asp Phe	Ala Leu Ser	Tyr Leu Glu	Ile Pro Asn	Arg Ile Glu	Phe	
	30	35		40		
tct att atg	gat cca aaa	aga aaa aca	aaa tgc taat	gaagcc atcas	gtcaa	651
Ser Ile Met	Asp Pro Lys	Arg Lys Thr	Lys Cys			
	45	50	55			
gggtcacatg	ccaataaaca	ataaattttc	cagaagaaat	gaaatccaac	tagacaaata	711
aagtagagct	tatgaaatgg	ttcagtaagg	atgagcttgt	tggtttttgt	tttgttttgt	771
tttgtttttt	taaagacgga	gtctcgctct	gtcactcagg	ctggagtgc	gtggtatgat	831
cttggctcac	tgtaacctcc	gcctcccggg	ttcaagccat	tctcctgcct	cagtctcctg	891
agtagctggg	attgcaggtg	cgtgccacca	tgcttggtta	atttttgtgt	tttggtaga	951
gacaggggtt	caccacgttg	gtcgggctgg	tctcgggctc	ctgacctctt	gatccgcctg	1011
ccttggcctc	ccaaagtgat	gggattacag	atgtgagcca	ccgtgcctag	ccaaggatga	1071

gattttttaa	gtatgttcca	gttctgtgtc	atggttggaa	gacagagtag	gaaggatatg	1131
gaaaagggtca	tggggaagca	gaggtgattc	atggctctgt	ggaatttgag	gtgaatggtt	1191
ccttattgtc	taggccactt	gtgaagaata	tgagtcagtt	attgccagcc	ttggaattta	1251
cttctctagc	ttacaatgga	cctttttgaa	ctgggaaaca	ccttgtctgc	attcacttta	1311
aaatgtcaaa	actaattttt	ataataaatg	tttattttca	catygaaaaa	aaaaaaaaaa	1370

<210> 48
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<220>
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 <222> 755..760

<221> polyA_site
 <222> 780..791
 <221> misc_feature
 <222> 361..531
 <223> homology
 id :W73841
 est

<221> misc_feature
 <222> 210..347
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 est

<221> misc_feature
 <222> 548..637
 <223> homology
 id :W73841
 est

<221> misc_feature
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<221> misc_feature
 <222> 361..530
 <223> homology
 id :HSU74317
 est

<221> misc_feature
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est

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<221> misc_feature
<222> 129..347
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<223> homology
id :AA044118
est

<221> misc_feature

<222> 176..347
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<221> misc_feature
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<221> misc_feature
 <222> 548..605
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 id :AA293342
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<221> misc_feature
 <222> 361..531
 <223> homology
 id :AA531561
 est

<221> misc_feature
 <222> 153..252
 <223> homology
 id :AA531561
 est

<400> 48

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gtgagctgct gagatttggg agtctgcgct aggcccgctt ggagttctga gccgatggaa      180
gagttcactc atg ttt gca ccc gcg gtg atg cgt gct ttt cgc aag aac          229
      Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn
              -30              -25              -20
aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg att gtt gga ggt          277
Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly
              -15              -10              -5
tct ttt ggt ctt cgt gag ttt tct caa atc cga tat gat gct gtg aag          325
Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys
              1              5              10
ggt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag aat aaa ata          373
Gly Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile
              15              20              25
tct tta gag tcg gaa tat gag aaa atc aaa gac tcc aag ttt gat gac          421
Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp
              30              35              40              45
tgg aag aat att cga gga ccc agg cct tgg gaa gat cct gac ctc ctc          469
Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu
              50              55              60
caa gga aga aat cca gaa agc ctt aag act aag aca act tgactctgct          518
Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
              65              70
gattctcttt tccttttttt ttttaaataa aaatactatt aactggactt cctaatatat          578
acttctatca agtggaaagg aaattccagg cccatggaaa cttggatatg ggtaatttgg          638
atggacaaaa ktaatctkct actaaaggct atgtaccagg tttttatact tcccagctaa          698
ttccatctgt ggatgaaagt tgcaatgttg gcccccgat kattttacac cntcgaaata          758

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<212> DNA
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<221> polyA_site
<222> 1420..1433

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<223> homology
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est

<221> misc_feature
<222> 268..697
<223> homology
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est

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<222> 582..687
<223> homology
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est

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est

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<222> 61..399
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est

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<221> misc_feature
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<221> misc_feature
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 <223> homology
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 est

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ctcaaacggc ctagtgcttc gcgcttcggg agaaaatcag cgggtctaatt aattcctctg      180
gtttgttgaa gcagttacca agaatcttca accctttccc acaaaagcta attgagtaca      240
cgttcctggt gagtacacgt tcctgttgat ttacaaaagg tgcaggatatg agcagggtctg      300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt      357
                                     Met Trp Trp Phe
                                     -20
cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
-15                               -10                               -5
gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata      453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
1                               5                               10                               15
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca gaa      501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Glu
20                               25                               30
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgc att      549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Ile
35                               40                               45
gct acc att tat gtt cgt tat aag caa gtt cat gct ctg agt cct gaa      597
Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala Leu Ser Pro Glu
50                               55                               60
gag aac gtt atc atc aaa tta aac aag gct ggc ctt gta ctt gga ata      645
Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu Val Leu Gly Ile
65                               70                               75
ctg agt tgt tta gga ctt tct att gtg gca aac ttc cag gaa aac aac      693
Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe Gln Glu Asn Asn
80                               85                               90                               95
cct ttt tgc tgc aca tgt aag tgg agc tgt gct tac ctt tgg tat ggg      741
Pro Phe Cys Cys Thr Cys Lys Trp Ser Cys Ala Tyr Leu Trp Tyr Gly
100                               105                               110

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```

ctc att ata tat gtt tgt tca gac cat cct ttc cta cca aaa tgc agc      789
Leu Ile Ile Tyr Val Cys Ser Asp His Pro Phe Leu Pro Lys Cys Ser
      115                      120                      125
cca aaa tcc aat ggc aaa aca agt ctt ctg gat cag act gtt gtt ggt      837
Pro Lys Ser Asn Gly Lys Thr Ser Leu Leu Asp Gln Thr Val Val Gly
      130                      135                      140
tat ctg gtg tgg agt aag tgc act tagcatgctg acttgctcat cagttttgca      891
Tyr Leu Val Trp Ser Lys Cys Thr
      145                      150
cagtggcaat tttgggactg atttagaaca gaaactccat tgggaaccccg aggacaaagg      951
ttatgcgctt cacatgatca ctactgcagc agaatggtct atgtcatttt ccttcttttg      1011
ttttttcctg acttacattc gtgattttca gaaaatttcc ttacgggtgg aagccaactt      1071
acatggatta accctctatg aactgcacc ttgccctatt aacaatgaac gaacacggct      1131
actttccags aagatattag atgaaaggat aaaatatttc tgtaantgan ttastgastt      1191
ctcagggant tggggaaang gttcacagaa gttgcttavl tottcatcrt gaanattttc      1251
aanccactta antcaaggct gacagstaac acgtgatgaa tgctgataat caggaaacat      1311
gaaagaagcc atttgcatag attattytaa aggatatcat caagaagamt attaaaaaca      1371
cctatgccta tactttttta tytcagaaaa taaagtcaaa agactatgaa aaaaaaaaaa      1431
aa                                                                1433

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<210> 50
<211> 1158
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 214..339
<223> Von Heijne matrix
      score 6.09999990463257
      seq AILLLQSQCAYWA/LP

<221> polyA_signal
<222> 1133..1138

<221> polyA_site
<222> 1146..1158

<221> misc_feature
<222> 840..968
<223> homology
      id :H64717
      est

<221> misc_feature
<222> 858..968
<223> homology
      id :H65208
      est

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<400> 50
aarttgagct tggggactgc agctgtgggg agatttcagt gcattgcctc ccctgggtgc      60
tcttcatctt ggatttgaaa gttgagagca gcatgttttg cccactgaaa ctcatcctgs      120
tgrsagtgtg mtggattatt ccttgggcct gaatgacttg aatgtttccc cgctgagct      180
aacagtccat gtgggtgatt cagctctgat ggg atg tgt ttt cca gag cac aga      234
                                Met Cys Phe Pro Glu His Arg
                                -40

```

```

aga caa atg tat att caa gat aga ctg gac tct gtc acc agg aga gca      282
Arg Gln Met Tyr Ile Gln Asp Arg Leu Asp Ser Val Thr Arg Arg Ala
-35          -30          -25          -20
cgc caa gga cga ata tgt gct ata cta tta ctc caa tct cag tgt gcc      330
Arg Gln Gly Arg Ile Cys Ala Ile Leu Leu Leu Gln Ser Gln Cys Ala
          -15          -10          -5
tat tgg gcg ctt cca gaa ccg cgt aca ctt gat ggg gga cat ctt atg      378
Tyr Trp Ala Leu Pro Glu Pro Arg Thr Leu Asp Gly Gly His Leu Met
          1          5          10
caa tgatggctct ctccctgctcc aagatgtgca agaggctgac cagggaaacct      431
Gln
atatctgtga aatccgcctc aaaggggaga gccaggtggt caagaaggcg gtggtactgc      491
atgtgcttcc agaggagccc aaaggtagcg aaatgcttac ttaaaggagg gccaaaggggc      551
aagagctttc atgtgcaaga ggcaaggaaa ctgattatct tgagtaaata ccagcctttg      611
ggctaagtac ttaccacaga gtgaatcttc aaagaaatga ntcattaaat tatttcagrt      671
cagaataaaa atakgagtta ttttagtta kaataaaata ttgataatta ttgtattatt      731
actttaaaaca cacttcccccc tcacaaaagc cctgtgaagg atgttttggt cacatataat      791
gtccaaatat gttttggaca catattttatt aaatggaata aatagtamtt gaaccctggc      851
accthtgaca acaaagtcoya tgtttTTTTT actatgccct aataccttts atcagttatc      911
cacattgatg ctacatytgt attttatagg taccctatgt taggtgtttt gggggataga      971
aaagaaataa gcagkycagg ctcaagtggct catgcctgta atcctagcat tttgggaggg      1031
tgaggcagca gaamtgcctg agccccaggg ttcaagactg cagtgaagcta tgawggcacc      1091
actgcattyt agcctgggwg acagagcaag actygtgtta aaataaaaaa agagaaaaaa      1151
aaaaaaa

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<210> 51
<211> 850
<212> DNA
<213> Homo sapiens

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<220>
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<222> 372..437
<223> Von Heijne matrix
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      seq LFLTCLFWPLAAL/NV

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<221> polyA_signal
<222> 812..817

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<221> polyA_site
<222> 838..850

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<222> 128..424
<223> homology
      id :N78012
      est

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<221> misc_feature
<222> 61..128
<223> homology
      id :N78012
      est

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<221> misc_feature
<222> 483..554

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<223> homology
    id :N78012
    est

<221> misc_feature
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<223> homology
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<222> 460..500
<223> homology
    id :N78012
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<221> misc_feature
<222> 577..612
<223> homology
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    est

<221> misc_feature
<222> 612..649
<223> homology
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<221> misc_feature
<222> 546..577
<223> homology
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    est

<221> misc_feature
<222> 29..63
<223> homology
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    est

<221> misc_feature
<222> 128..294
<223> homology
    id :W37233
    est

<221> misc_feature
<222> 370..509
<223> homology
    id :W37233
    est

<221> misc_feature
<222> 505..591
<223> homology
    id :W37233
    est

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<221> misc_feature
 <222> 293..330
 <223> homology
 id :W37233
 est

<221> misc_feature
 <222> 22..57
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 est

<221> misc_feature
 <222> 95..128
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 est

<221> misc_feature
 <222> 128..326
 <223> homology
 id :AA186399
 est

<221> misc_feature
 <222> 418..605
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 id :AA186399
 est

<221> misc_feature
 <222> 326..423
 <223> homology
 id :AA186399
 est

<221> misc_feature
 <222> 39..128
 <223> homology
 id :AA186399
 est

<221> misc_feature
 <222> 206..640
 <223> homology
 id :W52489
 est

<400> 51

agacacttcc	tggtgggac	cgagtggaggc	gacggggtag	gggttggcgc	tcaggcggcg	60
accatggcgt	atcacggcct	cactgtgcct	ctcattgtga	tgagcgtgtt	ctggggcttc	120
gtcggctttc	ttggtgcctt	ggttcattcc	taagggtcct	aaccggggag	ttatcattac	180
catgttggtg	acctgttcag	tttgctgcta	tctcttttgg	ctgattgcaa	ttctggccca	240
actcaaccct	ctctttggac	cgcaattgaa	aaatgaaacc	atctggtatc	tgaagtatca	300
ttggccttga	ggaagaagac	atgctctaca	gtgctcagtc	tttgagggtca	cgagaagaga	360
atgccttcta	g atg caa aat cac ctc	caa acc aga cca ctt ttc ttg act				410
	Met Gln Asn His Leu Gln Thr Arg Pro Leu Phe Leu Thr					
	-20	-15	-10			

tgc ctg ttt tgg cca tta gct gcc tta aac gtt aac agc aca ttt gaa	458
Cys Leu Phe Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu	
-5 1 5	
tgc ctt att cta caa tgc agc gtg ttt tcc ttt gcc ttt ttt gca ctt	506
Cys Leu Ile Leu Gln Cys Ser Val Phe Ser Phe Ala Phe Phe Ala Leu	
10 15 20	
tgg tgaattacgt gcctccataa cctgaactgt gccgactcca caaaacgatt	559
Trp	
atgtactctt ctgagataga agatgctgtt cttctgagag atacgttact ctctccttgg	619
aatctgtgga tttgaaaatg gctcctgcct tctcactgtg gaatcagtga agtggtttaga	679
aactgctgca agacaaacaa gactccagtg ggggtggtcag taggaaaaca cgttcagagg	739
gaagaaccat ctcaacagaa tcgcaccaa ctatactttc aggatgaatt tcttctttct	799
gccatctttt ggaataaata ttttcctcct ttytatgtaa aaaaaaaaaa a	850

<210> 52
 <211> 1107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 132..215
 <223> Von Heijne matrix
 score 3.59999990463257
 seq PLSDSWALLPASA/GV

<221> polyA_signal
 <222> 1069..1074

<221> polyA_site
 <222> 1094..1107

<221> misc_feature
 <222> 177..392
 <223> homology
 id :W80978
 est

<221> misc_feature
 <222> 425..542
 <223> homology
 id :W80978
 est

<221> misc_feature
 <222> 43..114
 <223> homology
 id :W80978
 est

<221> misc_feature
 <222> 387..441
 <223> homology
 id :W80978
 est

<221> misc_feature

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<222> 113..165
<223> homology
      id :W80978
      est

<221> misc_feature
<222> 551..590
<223> homology
      id :W80978
      est

<221> misc_feature
<222> 166..314
<223> homology
      id :AA043154
      est

<221> misc_feature
<222> 27..181
<223> homology
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      est

<221> misc_feature
<222> 425..564
<223> homology
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      est

<221> misc_feature
<222> 387..441
<223> homology
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      est

<221> misc_feature
<222> 309..352
<223> homology
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<221> misc_feature
<222> 549..580
<223> homology
      id :AA043154
      est

<221> misc_feature
<222> 601..1071
<223> homology
      id :AA126732
      est

<221> misc_feature
<222> 576..605
<223> homology
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      est

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<221> misc_feature
 <222> 387..477
 <223> homology
 id :AA161280
 est

<221> misc_feature
 <222> 292..362
 <223> homology
 id :AA161280
 est

<221> misc_feature
 <222> 46..113
 <223> homology
 id :AA161280
 est

<221> misc_feature
 <222> 217..277
 <223> homology
 id :AA161280
 est

<221> misc_feature
 <222> 113..160
 <223> homology
 id :AA161280
 est

<221> misc_feature
 <222> 173..217
 <223> homology
 id :AA161280
 est

<400> 52

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aacaacttcc ggccccactg agcgggtgtcc tgagccgatt acagctaggt agtggagcgc      60
cgctgcttac ctgggtgcag gagacagccg gagtcgctgg gggagctccg cgccgccgga      120
cgcccgtagac c atg tgg agg ctg ctg gct cgc gct agt gcg ccg ctc ctg      170
               Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu
               -25                               -20

cgg gtg ccc ttg tca gat tcc tgg gca ctc ctc ccc gcc agt gct ggc      218
Arg Val Pro Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly
-15                -10                -5                1
gta aag aca ctg ctc cca gta cca agt ttt gaa gat gtt tcc att cct      266
Val Lys Thr Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro
               5                10                15

gaa aaa ccc aag ctt aga ttt att gaa agg gca cca ctt gtg cca aaa      314
Glu Lys Pro Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys
               20                25                30

gta aga aga gaa cct aaa aat tta agt gac ata cgg gga cct tcc act      362
Val Arg Arg Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr
               35                40                45

gaa gct acg gag kkk aca gaa ggc aat ttt gca atc ttg gca ttg ggt      410
Glu Ala Thr Glu Xaa Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly
50                55                60                65

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ggt ggc tac ctg cat tgg ggc cac ttt gaa atg atg cgc ctg aca atc      458
Gly Gly Tyr Leu His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile
70                                75                                80
aac cgc tct atg gac ccc aag aac atg ttt gcc ata tgg cga gta cca      506
Asn Arg Ser Met Asp Pro Lys Asn Met Phe Ala Ile Trp Arg Val Pro
85                                90                                95
gcc cct ttc aag ccc atc act cgc aaa agt gtt ggg cat cgc atg ggg      554
Ala Pro Phe Lys Pro Ile Thr Arg Lys Ser Val Gly His Arg Met Gly
100                             105                             110
gga ggc aaa ggt gct att gac cac tac gtg aca cct gtg aag gct ggc      602
Gly Gly Lys Gly Ala Ile Asp His Tyr Val Thr Pro Val Lys Ala Gly
115                             120                             125
cgc mww gww gta gag atg ggt ggg cgt tgt gma ttt gaa gaa gtg caa      650
Arg Xaa Xaa Val Glu Met Gly Gly Arg Cys Xaa Phe Glu Glu Val Gln
130                             135                             140                             145
ggt ttc ctt gac cag gtt gcc cac aag ttg ccc tty gca gca aag gct      698
Gly Phe Leu Asp Gln Val Ala His Lys Leu Pro Phe Ala Ala Lys Ala
150                             155                             160
gtg agc cgc ggg act yta gag aag atg cga aaa gat caa gag gaa aga      746
Val Ser Arg Gly Thr Leu Glu Lys Met Arg Lys Asp Gln Glu Glu Arg
165                             170                             175
gaa mgt aac aac cag aac ccc tgg aca ttt gag cga ata gcc act gcc      794
Glu Xaa Asn Asn Gln Asn Pro Trp Thr Phe Glu Arg Ile Ala Thr Ala
180                             185                             190
mac atg ctg ggc ata cgg aaa gta ctg agc cca tat gac ttg acc cac      842
Xaa Met Leu Gly Ile Arg Lys Val Leu Ser Pro Tyr Asp Leu Thr His
195                             200                             205
aag ggg aaa tam tgg ggc aag tty tac atg ccc mam cgt gtg      884
Lys Gly Lys Xaa Trp Gly Lys Phe Tyr Met Pro Xaa Arg Val
210                             215                             220
tagtgagtgt aggagataac tgtatatagg stactgaaag aaggattytg catttytatt      944
ccctcagcc tacccactga agtytttggg tagctytaa gccataamta aggagcagca      1004
tttgagtaga ttttgaaaa acgatgttat ttgttgattt aaaaagaaaa cwgatatttt      1064
attaaataaa atttaaacat cacttcagga aaaaaaaaaa aaa                        1107

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<210> 53

<211> 500

<212> DNA

<213> Homo sapiens

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<221> sig_peptide

<222> 199..288

<223> Von Heijne matrix

score 5.59999990463257

seq IVSVLALIPETTT/LT

<221> polyA_signal

<222> 464..469

<221> polyA_site

<222> 489..500

<221> misc_feature

<222> 197..412

<223> homology

id :AA429945

est

<221> misc_feature
<222> 61..195
<223> homology
id :AA429945
est

<221> misc_feature
<222> 425..488
<223> homology
id :AA429945
est

<221> misc_feature
<222> 197..412
<223> homology
id :AA455042
est

<221> misc_feature
<222> 61..195
<223> homology
id :AA455042
est

<221> misc_feature
<222> 425..488
<223> homology
id :AA455042
est

<221> misc_feature
<222> 207..412
<223> homology
id :W93646
est

<221> misc_feature
<222> 58..195
<223> homology
id :W93646
est

<221> misc_feature
<222> 425..488
<223> homology
id :W93646
est

<221> misc_feature
<222> 197..412
<223> homology
id :AA516431
est

<221> misc_feature
<222> 90..195

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<223> homology
    id :AA516431
    est

<221> misc_feature
<222> 425..488
<223> homology
    id :AA516431
    est

<221> misc_feature
<222> 52..195
<223> homology
    id :W38899
    est

<221> misc_feature
<222> 197..324
<223> homology
    id :W38899
    est

<221> misc_feature
<222> 443..477
<223> homology
    id :W38899
    est

<221> misc_feature
<222> 197..338
<223> homology
    id :W52820
    est

<221> misc_feature
<222> 71..195
<223> homology
    id :W52820
    est

<221> misc_feature
<222> 339..401
<223> homology
    id :W52820
    est

<221> misc_feature
<222> 425..469
<223> homology
    id :W52820
    est

<221> misc_feature
<222> 40..195
<223> homology
    id :W19506
    est

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<400> 53
agagctgttnn cnsaagtagg ggagggcggt gctccgcmgm ggtggcggdh tgctatcgct      60
tcgcagaacc tactcaggca gccagctgag aagagttgag ggaaagtgct gctgctgggt      120
ctgcagacgc gatggataac gtgcagccga aaataaaaca tcgccccttc tgcttcagtg      180
tgaaaggcca cgtgayag atg ctg cgg ctg gat att atc aac tca ctg gta      231
                Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val
                -30                -25                -20
aca aca gta ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa      279
Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu
                -15                -10                -5
acc aca aca ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca      327
Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala
                1                5                10
gta tgc tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc      375
Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe
                15                20                25
aat ccc agc ggt cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa      423
Asn Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
                30                35                40                45
gtt ttg taattttata ttacttttta gtttgatact aagtattaaa catatttctg      479
Val Leu
tattcttcca aaaaaaaaaa a      500

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<210> 54

<211> 765

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 293..385

<223> Von Heijne matrix

score 4.40000009536743

seq TCCHLGLPHPVRA/PR

<221> polyA_signal

<222> 733..738

<221> polyA_site

<222> 752..765

<221> misc_feature

<222> 310..576

<223> homology

id :HUM426A07B

est

<400> 54

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aaacctgtgtt gctagggacc gggcggtttg cggcaaccgt gggcactgct gaatttgaat      60
tgagggggcga gggaaaagt ttctcaggt gtggtgggga gagggaggcg gatgccgng      120
aaaccgtagg kacgcggtca gaaaggcgac gggctgtcgg agttggaaag ggacgcctgg      180
tttcccccca agcgaaccgg gatgggaagt gacttcaatg agattgaact tcagctggat      240
tgaaagagag gctagaagtt ccgcttgcca gcagcctcct tagtagagcg ga atg agt      298
                Met Ser
                -30
aat acc cac acg gtg ctt gtc tca ctt ccc cat ccg cac ccg gcc ctc      346
Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro Ala Leu

```

	-25		-20		-15	
acc tgc tgt cac ctc ggc ctc cca cac ccg gtc cgc gct ccc cgc cct						394
Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro Arg Pro						
	-10		-5		1	
ctt cct cgc gta gaa ccg tgg gat cct agg tgg cag gac tca gag cta						442
Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser Glu Leu						
5	10		15			
agg tat cca cag gcc atg aat tcc ttc cta aat gag cgg tca tcg ccg						490
Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser Ser Pro						
20	25		30		35	
tgc agg acc tta agg caa gaa gca tcg gct gac aga tgt gat ctc						535
Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp Leu						
	40		45		50	
tgaacctgat agattgctga ttttatctta ttttatcctt gacttggtac aagttttggg						595
atttctgaaa agaccatata gataaccaca aatatcaaga aagtcgtctt cagtattaag						655
tagaatttag atttaggttt ccttcctgct tcccacctcc ttcgaataag gaaacgtctt						715
tgggaccaac tttatggaat aaataagctg agctgcaaaa waaaaaaaaa						765

<210> 55

<211> 584

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 130..189

<223> Von Heijne matrix

score 3.5

seq KFCLICLLTFIFH/HC

<221> polyA_signal

<222> 546..551

<221> polyA_site

<222> 572..584

<400> 55

aagacgcgcc ggtttctgcg acgcagttag cgcagttctgc tttggtgaat acacgatttg	60
gtgcagccgg ggtttggtac cgagcggaga ggagatgcac acggcactcg agtgtgagga	120
aaaatagaa atg aag gta cat atg cac aca aaa ttt tgc ctc att tgt ttg	171
Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu	
-20	-15
ctg aca ttt att ttt cat cat tgc aac cat tgc cat gaa gaa cat gac	219
Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp	
-5	1
cat ggc cct gaa gcg ctt cac aga cag cat cgt gga atg aca gaa ttg	267
His Gly Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu	
15	20
gag cca agc aaa ttt tca aag caa gct gct gaa aat gaa aaa aaa tac	315
Glu Pro Ser Lys Phe Ser Lys Gln Ala Glu Asn Glu Lys Lys Tyr	
30	35
tat att gaa aaa ctt ttt gag cgt tat ggt gaa aat gga aga tta tcc	363
Tyr Ile Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser	
45	50
ttt ttt ggt ttg gag aaa ctt tta aca aac ttg ggc ctt gga gag aga	411
Phe Phe Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu Arg	
60	65
	70


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aaa gta gtt gag att aat cat gag gat ctt ggc cac gat cat gtt tct      459
Lys Val Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val Ser
75          80          85          90
cat tta agg tat ttt ggc agt tca aga ggg aaa gca ttt tca ctc aca      507
His Leu Arg Tyr Phe Gly Ser Ser Arg Gly Lys Ala Phe Ser Leu Thr
          95          100          105
taaccaccca gcattcccat aatcatttaa attcagaaaa tcaaaactgt gaccagtgt      567
wtccacaaaa aaaaaaa                                     584

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<210> 56
<211> 1387
<212> DNA
<213> Homo sapiens

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<220>
<221> sig_peptide
<222> 191..325
<223> Von Heijne matrix
      score 4.59999990463257
      seq VLVYLVTAERVWS/DD

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<221> polyA_signal
<222> 1348..1353

<221> polyA_site
<222> 1374..1387

<221> misc_feature
<222> 1258..1372
<223> homology
      id :AA417826
      est

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<221> misc_feature
<222> 791..887
<223> homology
      id :AA417826
      est

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<221> misc_feature
<222> 94..524
<223> homology
      id :AA235826
      est

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<221> misc_feature
<222> 44..94
<223> homology
      id :AA235826
      est

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<221> misc_feature
<222> 1258..1372
<223> homology
      id :AA236941
      est

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<221> misc_feature
<222> 935..1279
<223> homology
      id :AA480326
      est

<221> misc_feature
<222> 1258..1372
<223> homology
      id :AA480326
      est

<221> misc_feature
<222> 724..1148
<223> homology
      id :AA234245
      est

<221> misc_feature
<222> 944..1279
<223> homology
      id :AA479344
      est

<221> misc_feature
<222> 1258..1372
<223> homology
      id :AA479344
      est

<221> misc_feature
<222> 1070..1212
<223> homology
      id :AA133636
      est

<221> misc_feature
<222> 1258..1372
<223> homology
      id :AA133636
      est

<221> misc_feature
<222> 938..1054
<223> homology
      id :AA133636
      est

<221> misc_feature
<222> 94..436
<223> homology
      id :AA133635
      est

<221> misc_feature
<222> 32..94
<223> homology
      id :AA133635

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est

<221> misc_feature
<222> 895..1273
<223> homology
id :AA479453
est

<221> misc_feature
<222> 1258..1371
<223> homology
id :AA253214
est

<221> misc_feature
<222> 94..268
<223> homology
id :AA482378
est

<400> 56

actcccaggc	tgggccagca	cacccggcag	gctctgtcct	ggaaacaggc	ttcaacgggc	60
ttccccgaaa	accttccccg	cttctggata	tgaavattca	agctgcttgc	tgagtcctat	120
tgccggctgc	tgggagccag	gagagccctg	aggagtagtc	actcagtagc	agctgacgcg	180
tgggtccacc	atg aac tgg agt atc ttt gag gga ctc ctg agt ggg gtc					229
	Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val					
	-45	-40	-35			
aac aag tac tcc aca gcc ttt ggg cgc atc tgg ctg tct ctg gtc ttc						277
Asn Lys Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe						
	-30	-25	-20			
atc ttc cgc gtg ctg gtg tac ctg gtg acg gcc gag cgt gtg tgg agt						325
Ile Phe Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser						
	-15	-10	-5			
gat gac cac aag gac ttc gac tgc aat act cgc cag ccc ggc tgc tcc						373
Asp Asp His Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser						
	1	5	10	15		
aac gtc tgc ttt gat gag ttc ttc cct gtg tcc cat gtg cgc ctc tgg						421
Asn Val Cys Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp						
	20	25	30			
gcc ctg cag ctt atc ctg gtg aca tgc ccc tca ctg ctc gtg gtc atg						469
Ala Leu Gln Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met						
	35	40	45			
cac gtg gcc tac cgg gag gtt cag gag aag agg cac cga gaa gcc cat						517
His Val Ala Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His						
	50	55	60			
ggg gag aac agt ggg cgc ctc tac ctg aac ccc ggc aag aar cgg ggt						565
Gly Glu Asn Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly						
	65	70	75	80		
ggg ctc tgg tgg aca tat gtc tgc agc cta gtg ttc aag gcg agc gtg						613
Gly Leu Trp Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val						
	85	90	95			
gac atc gcc ttt ctc tat gtg ttc cac tca ttc tac ccc aaa tat atc						661
Asp Ile Ala Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile						
	100	105	110			
ctc cct cct gtg gtc aag tgc cac gca gat cca tgt ccc aat ata gtg						709
Leu Pro Pro Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val						
	115	120	125			
gac tgc ttc atc tcc aag ccc tca gag aag aac att ttc acc ctc ttc						757

Asp Cys Phe Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe	
130 135 140	
atg gtg gcc aca gct gcc atc tgc atc ctg ctc aac ctc gtg gag ctc	805
Met Val Ala Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu	
145 150 155 160	
atc tac ctg gtg agc aag aga tgc cac gag tgc ctg gca gca agg aaa	853
Ile Tyr Leu Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys	
165 170 175	
gct caa gcc atg kgc aca ggt cat cac ccc cav gat acc acy ttt tcc	901
Ala Gln Ala Met Xaa Thr Gly His His Pro Xaa Asp Thr Thr Phe Ser	
180 185 190	
kgc aaa caa gas gac ytc ytt tcg ggk gac ytc atc ttt ctg ggn tca	949
Xaa Lys Gln Xaa Asp Xaa Xaa Ser Gly Asp Xaa Ile Phe Leu Gly Ser	
195 200 205	
gac agt cat cyt cct ytc tta cca gac cgc ccc cga gac cat gtg aag	997
Asp Ser His Xaa Pro Xaa Leu Pro Asp Arg Pro Arg Asp His Val Lys	
210 215 220	
aaa acc aty ttg tgaggggctg cctggamtgg tytggcaggt tgggcctgga	1049
Lys Thr Ile Leu	
225	
tggggaggct ytagcatyty tcataggtgc aacctgagag tgggggagct aagccatgag	1109
gtagggggcag gcaagagaga ggattcagac gytytgggag ccagttccta gtcctcaamt	1169
ccagccacct gccccagsth gacggcamtg ggccagtcc ccctytgsty tgcagstcgg	1229
tttcctttty tagaatggaa atagtgaggg ccaatgcca gggttggagg gaggagggcg	1289
ttcatagaag aacacacatg cgggcacct catygtgtgt ggccactgt cagaacttaa	1349
taaaagtcaa mtcatttgct gggttaaaaaa aaaaaaaaa	1387

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<210> 57
<211> 1385
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 141..251
<223> Von Heijne matrix
      score 4
      seq PLSLDCGHS LCRA/CI

<221> polyA_signal
<222> 1354..1359

<221> polyA_site
<222> 1375..1385

<221> misc_feature
<222> 1183..1240
<223> homology
      id :AA463623
      est

<221> misc_feature
<222> 176..239
<223> homology
      id :AA258927
      est

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<221> misc_feature
 <222> 803..854
 <223> homology
 id :AA286417
 est

<221> misc_feature
 <222> 1183..1213
 <223> homology
 id :AA608077
 est

<400> 57

aacaccacc	ctggcttttc	ttcacctctt	caaccaggag	ccgagatttc	tggtgctctg	60
aagccatcca	ggggtcttta	accagaagag	agaggagagc	ctcaggagtt	aggaccagaa	120
gaagccaggg	aagcagtgca	atg gct tca	aaa atc ttg	ctt aac gta	caa gag	173
		Met Ala Ser Lys	Ile Leu Leu	Asn Val Gln	Glu	
		-35		-30		
gag gtg acc	tgt ccc atc	tgc ctg gag	ctg ttg aca	gaa ccc ttg	agt	221
Glu Val Thr	Cys Pro Ile	Cys Leu Glu	Leu Leu Thr	Glu Pro Leu	Ser	
-25		-20		-15		
cta gac tgt	ggc cac agc	ctc tgc cga	gcc tgc atc	act gtg agc	aac	269
Leu Asp Cys	Gly His Ser	Leu Cys Arg	Ala Cys Ile	Thr Val Ser	Asn	
-10		-5	1	5		
aaag gag gca	gtg acc agc	atg gga gga	aaa agc agc	tgt cct gtg	tgt	317
Lys Glu Ala	Val Thr Ser	Met Gly Gly	Lys Ser Ser	Cys Pro Val	Cys	
	10	15	20			
gggt atc agt	tac tca ttt	gaa cat cta	cag gct aat	cag cat cgg	gcc	365
Gly Ile Ser	Tyr Ser Phe	Glu His Leu	Gln Ala Asn	Gln His Arg	Ala	
	25	30	35			
aac ata gtg	gag aga ctc	aag gag gtc	aag ttg agc	cca gac aat	ggg	413
Asn Ile Val	Glu Arg Leu	Lys Glu Val	Lys Leu Ser	Pro Asp Asn	Gly	
	40	45	50			
aaag aag aga	gat ctc tgt	gat cat cat	gga gag aaa	ctc cta ctc	ttc	461
Lys Lys Arg	Asp Leu Cys	Asp His His	Gly Glu Lys	Leu Leu Leu	Phe	
55	60	65	70			
tgt aag gag	gat agg aaa	gtc att tgc	tgg ctt tgt	gag cgg tct	cag	509
Cys Lys Glu	Asp Arg Lys	Val Ile Cys	Trp Leu Cys	Glu Arg Ser	Gln	
	75	80	85			
gag cac cgt	ggt cac cac	aca ggt cct	cac gga gga	agt att caa	gga	557
Glu His Arg	Gly His His	Thr Gly Pro	His Gly Gly	Ser Ile Gln	Gly	
	90	95	100			
atg tca gga	gaa act cca	ggc agt cct	caa gag gct	gaa gaa gga	aga	605
Met Ser Gly	Glu Thr Pro	Gly Ser Pro	Gln Glu Ala	Glu Glu Gly	Arg	
	105	110	115			
gga gga agc	tgagaagctg	gaagctgaca	tcagagaaga	gaaaacttcc		654
Gly Gly Ser						
120						
tggaagtatc	aggatacaaac	tgagagacaa	aggatacaaa	cagaatttga	tcagcttaga	714
agcatcctaa	ataatgagga	gcagagagag	ctgcaaagat	tggaagaaga	agaaaagaag	774
acgctggata	agtttgacaga	ggctgaggat	gagctagttc	agcagaagca	gttggtgaga	834
gagctcatct	cagatgtgga	gtgtcgaggt	cagtgggtcaa	caatggagct	gctgcaggac	894
atgagtggaa	tcatgaaatg	gagtgagatc	tggaggctga	aaaagccaaa	aatggtttcc	954
aagaaactga	agactgtatt	ccatgctcca	gatctgagta	ggatgctgcr	aatgttttaga	1014
ggaactgaca	gctgtccggt	gctactgggt	ggatgtcaca	ctgaattcag	tcaacctaaa	1074
tttgaatckt	gtccttttcag	aagatcagag	acaagtgata	tctgtgccaa	tttgaccttt	1134
tcagtgttat	aattatgggtg	tkbttgggat	cccaatatatt	btccststgg	gaaacattac	1194
tgggaagtgg	acgtgtccaa	gaaaactgcc	tggatcctgg	gggtatactg	tagaacatat	1254

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tcccgccata tgaagtatgt tgtagaaga tgtgcaaaty gtcaaaatbt ttacaccaa 1314
tacagacctc tatttggsa ctgggttata gggttacaga ataaatgtaa gtatggtgcc 1374
aaaaaaaaa a 1385
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<210> 58
<211> 1497
<212> DNA
<213> Homo sapiens
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<220>
<221> sig_peptide
<222> 212..268
<223> Von Heijne matrix
      score 8.60000038146973
      seq LLWLALACSPVHT/TL
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<221> polyA_signal
<222> 1465..1470
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<221> polyA_site
<222> 1489..1497
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<221> misc_feature
<222> 958..1110
<223> homology
      id :W72124
      est
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<221> misc_feature
<222> 1362..1488
<223> homology
      id :W72124
      est
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<221> misc_feature
<222> 1202..1312
<223> homology
      id :W72124
      est
```

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<221> misc_feature
<222> 1115..1190
<223> homology
      id :W72124
      est
```

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<221> misc_feature
<222> 1312..1370
<223> homology
      id :W72124
      est
```

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<221> misc_feature
<222> 653..942
<223> homology
      id :AA009415
      est
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<221> misc_feature
<222> 454..605
<223> homology
      id :AA009415
      est

<221> misc_feature
<222> 598..639
<223> homology
      id :AA009415
      est

<221> misc_feature
<222> 805..1032
<223> homology
      id :AA088502
      est

<221> misc_feature
<222> 633..807
<223> homology
      id :AA088502
      est

<221> misc_feature
<222> 598..639
<223> homology
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      est

<221> misc_feature
<222> 564..605
<223> homology
      id :AA088502
      est

<221> misc_feature
<222> 653..807
<223> homology
      id :AA181148
      est

<221> misc_feature
<222> 907..1046
<223> homology
      id :AA181148
      est

<221> misc_feature
<222> 475..605
<223> homology
      id :AA181148
      est

<221> misc_feature
<222> 598..639
<223> homology

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id :AA181148
est

<221> misc_feature
<222> 1069..1190
<223> homology
id :AA181149
est

<221> misc_feature
<222> 1362..1475
<223> homology
id :AA181149
est

<221> misc_feature
<222> 1202..1312
<223> homology
id :AA181149
est

<221> misc_feature
<222> 1312..1370
<223> homology
id :AA181149
est

<400> 58

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gcagatttcc	anssagaaga	cagagaagga	gcagtggtc	atggaatggg	ctgggggtcaa	120
agactgggtg	cctgggagct	gaggcagcca	ccgtttcagc	ctggccagcc	ctctggaccc	180
cgaggttgga	ccctactgtg	acacacctac	c atg cgg aca ctc ttc aac ctc			232
			Met Arg Thr Leu Phe Asn Leu			

-15

ctc tgg ctt gcc ctg gcc tgc agc cct gtt cac act acc ctg tca aag	280
Leu Trp Leu Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys	
-10 -5 1	

tca gat gcc asa aaa ccg cct caa aga cgc tgc tgg aga aga gtc agt	328
Ser Asp Ala Xaa Lys Pro Pro Gln Arg Arg Cys Trp Arg Arg Val Ser	
5 10 15 20	

ttt cag ata agc cgg tgc aar acc ggg gtt tgg tgg tgacggacct	374
Phe Gln Ile Ser Arg Cys Lys Thr Gly Val Trp Trp	
25 30	

caaagctgag	agtgtggttc	ttgagcatcg	cagctactgc	tcggcaaagg	cccgggacag	434
acactttgct	ggggatgtac	tgggctatgt	cactccatgg	aacagccatg	gctacgatgt	494
caccaaggtc	tttgggagca	agttcacaca	gatctcacc	gtctggctgc	agttgaagag	554
acgtggccgt	gagatgtttg	aggtcacggg	cctccacgac	gtggaccaag	ggtggatgcg	614
agctgtcagg	aagcatgcc	agggcctgca	catagtgcct	cggctcctgt	ttgaggactg	674
gacttacgat	gatttccgga	acgtcttaga	cagtgaggat	gagatagagg	agctgagcaa	734
gaccgtggtc	caggtggcaa	agaaccagca	tttcgatggc	ttcgtgggtg	aggtctggaa	794
ccagctgcta	agccagaagc	gcgtgggcct	catccacatg	ctcaccact	tggccgaggc	854
cctgcaccag	gcccggctgc	tggccctcct	ggtcatcccg	cctgccatca	ccccgggac	914
cgaccagctg	ggcatgttca	cgcacaagga	gtttgagcag	ctggcccccg	tgctggatgg	974
tttcagcctc	atgacctacg	actactctac	agcgcatcag	cctggcccta	atgcaccct	1034
gtcctgggtt	cgagcctgcg	tccaggtcct	ggaccgggaa	gtccaagtgg	cgaagcaaaa	1094
tctctctggg	gctcaacttc	tatggtatgg	actacgcgac	ctccaaggat	gcccgtgagc	1154
ctgttgtcgg	ggccaggtac	atccagacac	tgaadggacc	acaggccccg	ggaatggtgt	1214
gggacagcca	ggcctcagag	cacttcttcg	agtacaagaa	gagccgcagt	gggaggcacg	1274

tcgtcttcta	cccaaccctg	aagtcctgc	aggtgcgggc	tggagctggc	ccgggagctg	1334
ggcgttgggg	tctctatytg	ggagctgggc	cagggcctgg	actacttyta	cgacctgcty	1394
taggtgggca	ttgcggcctc	cgcggtggac	gtgttytttt	ytaagccatg	gagtgagtga	1454
gcaggtgtga	aatacaggcc	tccactccgt	ttgcaaaaaa	aaa		1497

<210> 59
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 147..248
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 score 4.30000019073486
 seq QLFAFLNLLPVEA/DI

<221> polyA_signal
 <222> 1538..1543

<221> polyA_site
 <222> 1558..1570

<221> misc_feature
 <222> 466..968
 <223> homology
 id :AA506103
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<221> misc_feature
 <222> 142..664
 <223> homology
 id :AA237105
 est

<221> misc_feature
 <222> 114..269
 <223> homology
 id :AA317201
 est

<221> misc_feature
 <222> 2..122
 <223> homology
 id :AA317201
 est

<221> misc_feature
 <222> 401..443
 <223> homology
 id :AA317201
 est

<221> misc_feature
 <222> 103..385
 <223> homology
 id :T80259

est

<221> misc_feature
<222> 21..120
<223> homology
id :T80259
est

<221> misc_feature
<222> 109..459
<223> homology
id :N32697
est

<221> misc_feature
<222> 45..87
<223> homology
id :N32697
est

<221> misc_feature
<222> 92..122
<223> homology
id :N32697
est

<221> misc_feature
<222> 1220..1409
<223> homology
id :AA449621
est

<221> misc_feature
<222> 928..1092
<223> homology
id :AA449621
est

<221> misc_feature
<222> 1178..1222
<223> homology
id :AA449621
est

<221> misc_feature
<222> 1220..1545
<223> homology
id :N34685
est

<221> misc_feature
<222> 1168..1222
<223> homology
id :N34685
est

<221> misc_feature
<222> 1220..1545

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<223> homology
      id :N22990
      est

<221> misc_feature
<222> 1178..1222
<223> homology
      id :N22990
      est

<221> misc_feature
<222> 114..325
<223> homology
      id :AA330462
      est

<221> misc_feature
<222> 18..122
<223> homology
      id :AA330462
      est

<221> misc_feature
<222> 135..475
<223> homology
      id :HUMEST5H12
      est

<400> 59
agtcgtccct gctagtactc cgggctgtgg gggtcgggtgc ggatattcag tcatgaaatc      60
agggtaggga cttctcccgc agcgacgcgg ctggcaagac tgtttgtgtt gcgggggccg      120
gaacttcaag gtgattttac aacgag atg ctg ctc tcc ata ggg atg ctc atg      173
                               Met Leu Leu Ser Ile Gly Met Leu Met
                               -30
ctg tca gcc aca caa gtc tac acc atc ttg act gtc cag ctc ttt gca      221
Leu Ser Ala Thr Gln Val Tyr Thr Ile Leu Thr Val Gln Leu Phe Ala
-25                               -20                               -10
ttc tta aac cta ctg cct gta gaa gca gac att tta gca tat aac ttt      269
Phe Leu Asn Leu Leu Pro Val Glu Ala Asp Ile Leu Ala Tyr Asn Phe
-5                               1                               5
gaa aat gca tct cag aca ttt gat gac ctc ccc gca ara ttt ggt tat      317
Glu Asn Ala Ser Gln Thr Phe Asp Asp Leu Pro Ala Xaa Phe Gly Tyr
10                               15                               20
aga ctt cca gct gaa ggt tta aag ggt ttt tta att aac tca aaa cca      365
Arg Leu Pro Ala Glu Gly Leu Lys Gly Phe Leu Ile Asn Ser Lys Pro
25                               30                               35
gag aat gcc tgt gaa ccc ata gtg cct cca cca gta aaa gac aat tca      413
Glu Asn Ala Cys Glu Pro Ile Val Pro Pro Pro Val Lys Asp Asn Ser
40                               45                               50                               55
tct ggc act ttc atc gtg tta att ara ara ctt gat tgt aat ttt gat      461
Ser Gly Thr Phe Ile Val Leu Ile Xaa Xaa Leu Asp Cys Asn Phe Asp
60                               65                               70
ata aag gtt tta aat gca cag aga gca gga tac aag gca gcc ata gtt      509
Ile Lys Val Leu Asn Ala Gln Arg Ala Gly Tyr Lys Ala Ala Ile Val
75                               80                               85
cac aat gtt gat tct gat gac ctc att agc atg gga tcc aac gac att      557
His Asn Val Asp Ser Asp Asp Leu Ile Ser Met Gly Ser Asn Asp Ile
90                               95                               100

```

gag gta cta aag aaa att gac att cca tct gtc ttt att ggt gaa tca	605
Glu Val Leu Lys Lys Ile Asp Ile Pro Ser Val Phe Ile Gly Glu Ser	
105 110 115	
tca gct agt tct ctg aaa gat gaa ttc aca tak gaa aaa ggg ggc cac	653
Ser Ala Ser Ser Leu Lys Asp Glu Phe Thr Xaa Glu Lys Gly Gly His	
120 125 130 135	
ctt atc tta gtt cca gaa ttt agt ctt cct ttg gaa tac tac cta att	701
Leu Ile Leu Val Pro Glu Phe Ser Leu Pro Leu Glu Tyr Tyr Leu Ile	
140 145 150	
ccc ttc ctt atc atr gtg ggc atc tgt ctc atc ttg ata gtc att ttc	749
Pro Phe Leu Ile Xaa Val Gly Ile Cys Leu Ile Leu Ile Val Ile Phe	
155 160 165	
atg atc aca aaa ttg tcc agg gat aga cat aga gct aga aac aga	797
Met Ile Thr Lys Leu Ser Arg Asp Arg His Arg Ala Arg Arg Asn Arg	
170 175 180	
ctt cgt aaa gat caa ctt aag aaa ctt cct gta cat aaa ttc aag aaa	845
Leu Arg Lys Asp Gln Leu Lys Lys Leu Pro Val His Lys Phe Lys Lys	
185 190 195	
gga gat gag tat gat gta tgt gcc att tgt ttg gat gag tat gaa gat	893
Gly Asp Glu Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr Glu Asp	
200 205 210 215	
gga gac aaa ctc aga atc ctt ccc tgt tcc cat gct tat cat tgc aag	941
Gly Asp Lys Leu Arg Ile Leu Pro Cys Ser His Ala Tyr His Cys Lys	
220 225 230	
tgt gta gac cct tgg cta act aaa acc aaa acc tgt cca gtg tgc	989
Cys Val Asp Pro Trp Leu Thr Lys Thr Lys Lys Thr Cys Pro Val Cys	
235 240 245	
agg caa aaa gtt gtt cct tct caa ggc gat tca gac tct gac aca gac	1037
Arg Gln Lys Val Val Pro Ser Gln Gly Asp Ser Asp Ser Asp Thr Asp	
250 255 260	
agt agt caa gaa gaa aat gaa gtg aca gaa cat acc cct tta ctg aga	1085
Ser Ser Gln Glu Glu Asn Glu Val Thr Glu His Thr Pro Leu Leu Arg	
265 270 275	
cct tta gnc ttc tgt cag tgc cca rgt cam ttt ggg gct tta ntc gga	1133
Pro Leu Xaa Phe Cys Gln Cys Pro Xaa Xaa Phe Gly Ala Leu Xaa Gly	
280 285 290 295	
ant ccc gct cac ant cag aak cat gac aga atc att cag act ast gag	1181
Xaa Pro Ala His Xaa Gln Xaa His Asp Arg Ile Ile Gln Thr Xaa Glu	
300 305 310	
gaa gac gac aat gaa gat act gac agt agt gat gca gaa gaa	1223
Glu Asp Asp Asn Glu Asp Thr Asp Ser Asp Ala Glu Glu	
315 320 325	
tgaaattaat gaacatgatg tcgtgggtcca gttgcagcct aatgggtgaac gggattacaa	1283
catagcaaat actgtttgac tttcagaaga tgattggttt atttcccttt aaaatgatta	1343
ggtatatact gtaatttgat tttttgctcc cttaaaagat ttytgtagaa ataacttatt	1403
ttttagtact ytacagttta atcaaattac tgaaacagga cttttgatyt ggtattttatc	1463
tgccaagaat atacttcatt cactaataat agactggtgc tgtaactcaa gcatcaattc	1523
agctytytytt ttggaatgaa agtatagcca aaacaaaaaa aaaaaaa	1570

<210> 60

<211> 1022

<212> DNA

<213> Homo sapiens

<220>

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<222> 112..237

<223> Von Heijne matrix
 score 7.19999980926514
 seq ILFSLSFLLVIIIT/FP

<221> polyA_signal
 <222> 976..981

<221> polyA_site
 <222> 1010..1022

<400> 60

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agctccaaac ccatgaaaaa ttgccaagta taaaagcttc tcaagaatga g atg gat	117
	Met Asp
tct agg gtg tct tca cct gag aag caa gat aaa gag aat ttc gtg ggt	165
Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe Val Gly	
-40 -35 -30 -25	
gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg atc ctg ttt tcc ctc	213
Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe Ser Leu	
-20 -15 -10	
tct ttc ctg ttg gtg atc att acc ttc ccc atc tcc ata tgg atg tgc	261
Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp Met Cys	
-5 1 5	
ttg aag atc att aag gag tat gaa cgt gct gtt gta ttc cgt ctg gga	309
Leu Lys Ile Ile Lys Glu Tyr Glu Arg Ala Val Val Phe Arg Leu Gly	
10 15 20	
cgc atc caa gct gac aaa gcc aag ggg cca ggt ttg atc ctg gtc ctg	357
Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro Gly Leu Ile Leu Val Leu	
25 30 35 40	
cca tgc ata gat gtg ttt gtc aag gtt gac ctc cga aca gtt act tgc	405
Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu Arg Thr Val Thr Cys	
45 50 55	
aac att cct cca caa gag atc ctc acc aga gac tcc gta act act cag	453
Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp Ser Val Thr Thr Gln	
60 65 70	
gta gat gga gtt gtc tat tac aga atc tat agt gct gtc tca gca gtg	501
Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser Ala Val Ser Ala Val	
75 80 85	
gct aat gtc aac gat gtc cat caa gca aca ttt ctg ctg gct caa acc	549
Ala Asn Val Asn Asp Val His Gln Ala Thr Phe Leu Leu Ala Gln Thr	
90 95 100	
act ctg aga aat gtc tta ggg aca cag acc ttg tcc cag atc tta gct	597
Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile Leu Ala	
105 110 115 120	
gga cga gaa gag atc gcc cat agc atc cag act tta ctt gat gat gcc	645
Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp Asp Ala	
125 130 135	
acc gaa ctg tgg ggg atc cgg gtg gcc cga gtg gaa atc aaa gat gtt	693
Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys Asp Val	
140 145 150	
cgg att ccc gtg cag ttg cag aga tcc atg gca gcc gag gct gag gcc	741
Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala Glu Ala	
155 160 165	
acc cgg gaa gcg aga gcc aag gtc ctt gca gct gaa gga gaa atg agt	789
Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu Met Ser	
170 175 180	
gct tcc aaa tcc ctg aag tca gcc tcc atg gtg ctg gct gag tct ccc	837
Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu Ser Pro	

185	190	195	200	
ata gct ctc cag ctg cgc tac ctg cag acc ttg agc acg gta gcc acc				885
Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val Ala Thr				
	205	210	215	
gag aag aat tct acg att gtg ttt cct ctg ccc atg aat ata cta gag				933
Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile Leu Glu				
	220	225	230	
ggc att ggt ggc gtc agc tat gat aac cac aag aag ctt cca aat aaa				981
Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro Asn Lys				
	235	240	245	
gcc tgaggtcctc ttgcggtagt cagctaaaaa aaaaaaaa				1022
Ala				

<210> 61
 <211> 615
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> Von Heijne matrix
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<221> polyA_signal
 <222> 586..591

<221> polyA_site
 <222> 603..615

<221> misc_feature
 <222> 341..574
 <223> homology
 id :AA453275
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 <222> 174..332
 <223> homology
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 est

<221> misc_feature
 <222> 85..171
 <223> homology
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<221> misc_feature
 <222> 341..574
 <223> homology
 id :AA149631
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<221> misc_feature
 <222> 170..339

<223> homology
id :AA149631
est

<221> misc_feature
<222> 43..123
<223> homology
id :AA149631
est

<221> misc_feature
<222> 88..339
<223> homology
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<221> misc_feature
<222> 1..345
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<221> misc_feature
<222> 341..574
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
<222> 59..338
<223> homology
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      est

<221> misc_feature
<222> 344..415
<223> homology
      id :AA131842
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<221> misc_feature
<222> 400..434
<223> homology
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<221> misc_feature
<222> 341..574
<223> homology
      id :AA152042
      est

<221> misc_feature
<222> 183..339
<223> homology
      id :AA152042
      est

<400> 61
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gatcctgcca acattgttca tgactttaac aagaaactta cagcctatctt agatcttaac      120
ctggataagt gctatgtgat ccctctgaac acttccattg ttatgccacc cagaaaccta      180
ctggagttac ttattaacat caaggctgga acctatttgc ctcagtccta tctgattc      238
atg agc aca tgg tta tta ctg atc gca ttg aaa aca ttg atc acc tgg      286
Met Ser Thr Trp Leu Leu Leu Ile Ala Leu Lys Thr Leu Ile Thr Trp
-25 -20 -15
gtt tct tta ttt atc gac tgt gtc atg aca agg aaa ctt aca aac tgc      334
Val Ser Leu Phe Ile Asp Cys Val Met Thr Arg Lys Leu Thr Asn Cys
-10 -5 1 5
aac gct aga gaa act att aaa ggt att cag aaa cgt gaa gcc agc aat      382
Asn Ala Arg Glu Thr Ile Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn
10 15 20
tgt ttc gca att cgg cat ttt gaa aac aaa ttt gcc gtg gaa act tta      430
Cys Phe Ala Ile Arg His Phe Glu Asn Lys Phe Ala Val Glu Thr Leu
25 30 35
att tgt tct tgaacagtca agaaaaacat tattgaggaa aattaatatc      479
Ile Cys Ser
40
acagcataac cccacccttt acattttgtg cagtgattat tttttaaagt cttctttcat      539
gtaagtagca aacagggctt tactatcttt tcatctcatt aattcaatta aaaccattac      599

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615

<210> 62
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<212> DNA
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<221> polyA_signal
<222> 771..776

<221> polyA_site
<222> 791..804

<221> misc_feature
<222> 244..789
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<221> misc_feature
<222> 286..790
<223> homology
id :AA236527
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<221> misc_feature
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<223> homology
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<221> misc_feature
<222> 520..790
<223> homology
id :AA165350
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<221> misc_feature
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<223> homology
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<221> misc_feature
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<221> misc_feature

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<222> 326..790
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<221> misc_feature
<222> 326..790
<223> homology
      id :AA490310
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<221> misc_feature
<222> 515..780
<223> homology
      id :AA164559
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<221> misc_feature
<222> 325..522
<223> homology
      id :AA164559
      est

<221> misc_feature
<222> 350..790
<223> homology
      id :AA427895
      est

<221> misc_feature
<222> 378..790
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      id :AA532390
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<222> 186..382
<223> homology
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      est

<221> misc_feature
<222> 61..141
<223> homology
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      est

<221> misc_feature
<222> 426..478
<223> homology
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<221> misc_feature
<222> 29..61
<223> homology
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      est

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<221> misc_feature
 <222> 389..790
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<221> misc_feature
 <222> 425..790
 <223> homology
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<221> misc_feature
 <222> 186..430
 <223> homology
 id :AA428006
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<221> misc_feature
 <222> 59..132
 <223> homology
 id :AA428006
 est

<400> 62

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aacagcgggc agggaaagcc gcggaaggg tactccaggc gagaggcgga cgcgagtcgt      60
cgtggcagga aaagtgacta gtcctcccttc gttgtcagcc agggacgaga acacagccac      120
gctcccaccc ggctgcchaa ggatccctcg gcggcg atg tcg gcc gcc ggt gcc      174
                               Met Ser Ala Ala Gly Ala
                               -60
cga ggc ctg cgg gcc acc tac cac cgg ctc ctc gat aaa gtg gag ctg      222
Arg Gly Leu Arg Ala Thr Tyr His Arg Leu Leu Asp Lys Val Glu Leu
-55 -50 -45
atg ctg ccc gag aaa ttg agg ccg ttg tac aac cat cca gca ggt ccc      270
Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro
-40 -35 -30
aga aca gtt ttc ttc tgg gct cca att atg aaa tgg ggg ttg gtg tgt      318
Arg Thr Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys
-25 -20 -15 -10
gct gga ttg gct gat atg gcc aga cct gca gaa aaa ctt agc aca gct      366
Ala Gly Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala
-5 1 5
caa tct gct gtt ttg atg gct aca ggg ttt att tgg tca aga tac tca      414
Gln Ser Ala Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser
10 15 20
ctt gta att att ccg aaa aat tgg agt ctg ttt gct gtt aat ttc ttt      462
Leu Val Ile Ile Pro Lys Asn Trp Ser Leu Phe Ala Val Asn Phe Phe
25 30 35
gtg ggg gca gca gga gcc tct cag ctt ttt cgt att tgg aga tat aac      510
Val Gly Ala Ala Gly Ala Ser Gln Leu Phe Arg Ile Trp Arg Tyr Asn
40 45 50 55
caa gaa cta aaa gct aaa gca cac aaa taaaagagtt cctgatcacc      557
Gln Glu Leu Lys Ala Lys Ala His Lys
60
tgaacaatct agatgtggac aaaaccattg ggacctagtt tattatttgg ttattgataa      617
agcaaagcta actgtgtgtt tagaaggcac tgtaactggg agctagttct tgattcaata      677
gaaaaatgca gcaaactttt aataacagtc tctctacatg acttaaggaa cttatctatg      737

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gatattagta acatttttct accatttgct cgtaataaaa catacttgct cgtaaaaaaa 797
aaaaaaa 804

<210> 63
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<220>
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score 12.3999996185303
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<221> polyA_signal
<222> 768..773

<221> polyA_site
<222> 780..792

<221> misc_feature
<222> 154..428
<223> homology
id :R22491
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<221> misc_feature
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<223> homology
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<221> misc_feature
<222> 47..218
<223> homology
id :AA136163
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<221> misc_feature
<222> 265..403
<223> homology
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<221> misc_feature
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<222> 123..265
<223> homology
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<221> misc_feature
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<221> misc_feature
<222> 128..403
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<221> misc_feature
<222> 138..403
<223> homology
id :AA314807
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<221> misc_feature
<222> 164..403
<223> homology
id :AA271811
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<221> misc_feature
<222> 163..385
<223> homology
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<221> misc_feature
<222> 154..403
<223> homology
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<221> misc_feature
<222> 2..250
<223> homology
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<221> misc_feature
<222> 154..403
<223> homology
id :AA470189
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<221> misc_feature
<222> 217..403
<223> homology
id :AA462839

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<221> misc_feature
<222> 154..403
<223> homology
id :AA120322
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<221> misc_feature
<222> 163..403
<223> homology
id :W71694
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<221> misc_feature
<222> 164..385
<223> homology
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<221> misc_feature
<222> 266..403
<223> homology
id :AA036242
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<400> 63

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cagccctgct ccctgcagcc aggtgtagtt tcgggagcca ctggggccaa agtgagagtc	120
cagcgggtcct ccagcgcttg ggccacggcg gcggccctgg gagcagaggt ggagcgaccc	180
cattacgcta aag atg aaa ggc tgg ggt tgg ctg gcc ctg ctt ctg ggg	229
Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly	
-20 -15 -10	
gcc ctg ctg gga acc gcc tgg gct cgg agg agc cgg gat ctc cac tgt	277
Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Arg Asp Leu His Cys	
-5 1 5	
gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa att gcc cag	325
Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln	
10 15 20	
gtg gac ccc aag aag acc att cag atg gga tcc ttc cgg atc aat cca	373
Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro	
25 30 35 40	
gat ggc agc cag tca gtg gtg gag gta act gtt act gkt tcc ccc aaa	421
Asp Gly Ser Gln Ser Val Val Glu Val Thr Val Thr Xaa Ser Pro Lys	
45 50 55	
aca aaa gta gct cac tct ggc ttt tgg atg aaa att cga ctg ctt aaa	469
Thr Lys Val Ala His Ser Gly Phe Trp Met Lys Ile Arg Leu Leu Lys	
60 65 70	
aaa gga cct tgg tct taatagaaaa tgaagraaaa cagactcaga aaaaaagatt	524
Lys Gly Pro Trp Ser	
75	
tbggctctgt ctcawtttgg aagaaggctg gcaggcttat tccccaatgc aactttgctt	584
cctggctgca aaccyttaat acytttgttt ctgctgtaga aatttgtag ccaaaacawg	644
ggagtcctga twcagcaacc cttcttcca caatccacca tgactggttt ttaatgtamc	704
acttggggta tacatgcaaa accatccggt cmaaaatctg aatycggagc ttaaaaattt	764
aaaaatgaaa aacchaaaaa aaaaaaaa	792

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<210> 64
<211> 832
<212> DNA
<213> Homo sapiens

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<221> sig_peptide
<222> 148..207
<223> Von Heijne matrix
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<221> polyA_signal
<222> 789..794

<221> polyA_site
<222> 820..832

<221> misc_feature
<222> 258..553
<223> homology
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      est

<221> misc_feature
<222> 117..219
<223> homology
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<221> misc_feature
<222> 552..645
<223> homology
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<221> misc_feature
<222> 217..258
<223> homology
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<221> misc_feature
<222> 258..553
<223> homology
      id :AA314807
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<221> misc_feature
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<221> misc_feature
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<223> homology
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est

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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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<223> homology
id :AA136163
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aggtggagcg accccattac gctaaag atg aaa ggc tgg ggt tgg ctg gcc ctg      174
                               Met Lys Gly Trp Gly Trp Leu Ala Leu
                               -20                               -15
ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat      222
Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
-10                               -5                               1                               5
ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa act aga atg gga      270
Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Thr Arg Met Gly
10                               15                               20
aat tgc cca ggt gga ccc caa gaa gac cat tca gat ggg atc ttt ccg      318
Asn Cys Pro Gly Gly Pro Gln Glu Asp His Ser Asp Gly Ile Phe Pro
25                               30                               35
gat caa tcc aga tgg cag cca gtc agt ggt gga ggt gcc tta tgc ccg      366
Asp Gln Ser Arg Trp Gln Pro Val Ser Gly Gly Gly Ala Leu Cys Pro
40                               45                               50
ctc aga ggc cca cct cac aga gct gct gga gga gat atg tgaccggatg      415
Leu Arg Gly Pro Pro His Arg Ala Ala Gly Gly Asp Met
55                               60                               65
aaggagtatg gggaacagat tgatccttcc acccatcgca agaactacgt acgtgtagtg      475
ggccggaatg gagaatccag tgaactggac ctacaaggca tccgaatcga ctgagatatt      535
agcggcaccc tcaagbtttg cgtgtgggaa cattgtggag gaatacaggg atgaactcat      595
tgaattcttt tcccagagagg ctgacaatgt taaagacaaa ctttgcagta agcgaacaga      655
tctttgtgac catgccctgc acatatcggc atgatgagct atgaaccact ggagcagccc      715
acactggctt gatggatcac ccccaggnaa gggaaaatgg tggcaatgcc ttttatatat      775
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<210> 65
<211> 721
<212> DNA
<213> Homo sapiens

<220>

<221> sig_peptide
<222> 156..230
<223> Von Heijne matrix
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<221> polyA_signal
<222> 706..711

<221> polyA_site
<222> 709..721

<221> misc_feature
<222> 351..688
<223> homology
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<221> misc_feature
<222> 289..353
<223> homology
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<221> misc_feature
<222> 274..641
<223> homology
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<221> misc_feature
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<223> homology
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<221> misc_feature
<222> 242..641
<223> homology
id :AA143192
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<221> misc_feature
<222> 261..646
<223> homology
id :AA594850
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<221> misc_feature
<222> 165..474
<223> homology
id :AA563681
est

<221> misc_feature
<222> 1..74
<223> homology
id :AA563681

est

<221> misc_feature
<222> 261..643
<223> homology
id :AA287457
est

<221> misc_feature
<222> 352..646
<223> homology
id :N22567
est

<221> misc_feature
<222> 299..354
<223> homology
id :N22567
est

<221> misc_feature
<222> 265..303
<223> homology
id :N22567
est

<221> misc_feature
<222> 30..165
<223> homology
id :AA186657
est

<221> misc_feature
<222> 270..349
<223> homology
id :AA186657
est

<221> misc_feature
<222> 213..261
<223> homology
id :AA186657
est

<221> misc_feature
<222> 165..214
<223> homology
id :AA186657
est

<221> misc_feature
<222> 346..387
<223> homology
id :AA186657
est

<221> misc_feature
<222> 52..400

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<223> homology
      id :HSC1ED081
      est

<221> misc_feature
<222> 398..436
<223> homology
      id :HSC1ED081
      est

<221> misc_feature
<222> 171..316
<223> homology
      id :AA143136
      est

<400> 65
atatttgggtc cggcctgctc gcmgtccgct ccgctccgcc ttagacctgt tgcccagcat      60
cctgcagtt  cgcgwacag tctctattag agcgctgta tagaggcaga kaggagtga      120
gtccacagtt cctctcctcc tagagcctgc cgacc atg ccc gcg ggc gtg ccc      173
                               Met Pro Ala Gly Val Pro
                               -25                               -20
atg tcc acc tac ctg aaa atg ttc gca gcc agt ctc ctg gcc atg tgc      221
Met Ser Thr Tyr Leu Lys Met Phe Ala Ala Ser Leu Leu Ala Met Cys
                               -15                               -10                               -5
gca ggg gca gaa gtg gtg cac agg tac tac cga ccg gac ctg aca ata      269
Ala Gly Ala Glu Val Val His Arg Tyr Tyr Arg Pro Asp Leu Thr Ile
                               1                               5                               10
cct gaa att cca cca aag cgt gga gaa ctc aaa acg gag ctt ttg gga      317
Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu Lys Thr Glu Leu Leu Gly
                               15                               20                               25
ctg aaa gaa aga aaa cac aaa cct caa gtt tct caa cag gag gaa ctt      365
Leu Lys Glu Arg Lys His Lys Pro Gln Val Ser Gln Gln Glu Glu Leu
                               30                               35                               40                               45
aaa taactatgcc aagaattctg tgaataatat aagtcttaaa tatgtatttc      418
Lys
ttaattttatt gcatcaaact acttgtcctt aagcacttag tctaagtcta actgcaagag      478
gaggtgctca gtggatgttt agccgatacg ttgaaattta attacggttt gattgatatt      538
tcttgaaaac tgccaaagca catatcatca aaccatttca tgaatatggt ttggaagatg      598
tttagtcttg aatataacgc gaaatagaat atttgtaagt ctactatatg gggtgtcttt      658
atttcatata aattaagaaa ttatttaaaa actatgaact aggtttcatt aaaaaaaaaa      718
gaa                                                                    721

<210> 66
<211> 531
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 272..397
<223> Von Heijne matrix
      score 4.59999990463257
      seq RIPS L P G S P V C W A / W P

<221> polyA_signal
<222> 503..508

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<221> polyA_site
<222> 518..531

<221> misc_feature
<222> 235..517
<223> homology
      id :AA524403
      est

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<221> misc_feature
<222> 52..208
<223> homology
      id :AA524403
      est

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<221> misc_feature
<222> 259..517
<223> homology
      id :N93600
      est

```

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<221> misc_feature
<222> 85..207
<223> homology
      id :N93600
      est

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```

<221> misc_feature
<222> 353..517
<223> homology
      id :AA594610
      est

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```

<221> misc_feature
<222> 258..363
<223> homology
      id :AA594610
      est

```

```

<221> misc_feature
<222> 105..207
<223> homology
      id :AA594610
      est

```

```

<221> misc_feature
<222> 202..517
<223> homology
      id :AA074748
      est

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<221> misc_feature
<222> 116..153
<223> homology
      id :AA074748
      est

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<221> misc_feature
<222> 167..202
<223> homology
id :AA074748
est

<221> misc_feature
<222> 258..517
<223> homology
id :N93603
est

<221> misc_feature
<222> 208..251
<223> homology
id :N93603
est

<221> misc_feature
<222> 163..202
<223> homology
id :N93603
est

<221> misc_feature
<222> 90..125
<223> homology
id :N93603
est

<221> misc_feature
<222> 125..363
<223> homology
id :HSPD04938
est

<221> misc_feature
<222> 353..517
<223> homology
id :HSPD04938
est

<221> misc_feature
<222> 28..227
<223> homology
id :AA074804
est

<221> misc_feature
<222> 265..310
<223> homology
id :AA074804
est

<221> misc_feature
<222> 227..263
<223> homology
id :AA074804

est

<221> misc_feature
<222> 352..385
<223> homology
id :AA074804
est

<400> 66

aaaaggaag aggtysggag cgctcgcgag atctcggacc acccaacctg aaaggtgctt 60
aggaagtga aagggccaga ggaggcctcc gggcaaatgg ccggagctgg accgacctg 120
ctgctacgag aagagaatgg ctgttgcaagt cggcgtcaga gcagctccag tgccggggat 180
tcggacggag agcgcgagga ctcggcggtt gagcgcgccc gacagcagct agagcgctg 240
ctcaacaaga ctatgcgcat tcgcatgaca g atg gac gga cac tgg tgc gct 292

Met Asp Gly His Trp Ser Ala
-40

gct ttc tct gca ctg acc gtg act gca atg tca tcc tgg gct cgg cgc 340
Ala Phe Ser Ala Leu Thr Val Thr Ala Met Ser Ser Trp Ala Arg Arg
-35 -30 -25 -20

agg agt tcc tca agc cgt cgg att cct tct ctg ccg ggg agc ccc gtg 388
Arg Ser Ser Ser Ser Arg Arg Ile Pro Ser Leu Pro Gly Ser Pro Val
-15 -10 -5

ttgc tgg gcc tgg cca tgg tac ccg gac acc aca tgc ttt cca ttg agg 436
Cys Trp Ala Trp Pro Trp Tyr Pro Asp Thr Thr Ser Phe Pro Leu Arg

1 5 10
ttgc aga ggg aga gtc tgaccggggc tccgtatctc tgaccacgat ggcgcttacc 491
Cys Arg Gly Arg Val
15

tttcagactt cattaaactt atgaccaaaa aaaaaaaaaa 531

<210> 67
<211> 783
<212> DNA
<213> Homo sapiens

<220>

<221> sig_peptide
<222> 381..629
<223> Von Heijne matrix
score 8.60000038146973
seq LELLTSCSPASA/SQ

<221> polyA_signal
<222> 736..741

<221> polyA_site
<222> 770..783

<221> misc_feature
<222> 207..263
<223> homology
id :AA357230
est

<400> 67

agggacttcc ggctcgctg gcgtggacgt ttgtggtggg gcgtggtggt ccgcgctctc 60
agaactgtgc tgggaaggat ggtagggcga ctggggctca cctccgcacc gttgtaggac 120

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ccggggtagg gttttgagcc cgtgggagct gccccacgcg gcctcgctct gccaacggtc 180
ggatggcgga gacgaaggac gcagcgcaga tggttggtgac cttcaaggat gtggctgtga 240
cctttaccog ggaggagtgg agacagctgg acctggccca gaggaccctg taccgagagg 300
tgatcgggtt cccaaaccag agttgggtcca cctgctagag catgggcagg agctgtggat 360
agtgaagaga ggcctctcac atg cta cct gtg cag agt ttc act ctt gtt gcc 413
                Met Leu Pro Val Gln Ser Phe Thr Leu Val Ala
                        -80                                -75
cag gct gga gtg cag tgg cgc cat ctc agc tca ctg caa ctt ctg cct 461
Gln Ala Gly Val Gln Trp Arg His Leu Ser Ser Leu Gln Leu Leu Pro
      -70                                -60
ccc gag ttc aag gga ttc tcc tgc ctc agc ctc ccg agt agc tgg gat 509
Pro Glu Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp
      -55                                -45
tac agg cgc cca cca cca tgc ccg gct ggt ttt ttt gta ttt tta gta 557
Tyr Arg Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val
      -40                                -35                                -30                                -25
gag acg ggg ctt cac cat gtt ggc cag gct ggt ctt gaa ctc ttg acc 605
Glu Thr Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr
      -20                                -15                                -10
tca tgt agt cca ccc gcc tct gcc tcc caa agt gct gcg att aca ggc 653
Ser Cys Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly
      -5                                1                                5
gtg agc cac gtg ccc ggc aaa aaa aaa ctg ctt aag gtt gaa aag aaa 701
Val Ser His Val Pro Gly Lys Lys Lys Leu Leu Lys Val Glu Lys Lys
      10                                15                                20
aat tta aga aaw ttg ctg acg gra ata aaa acy taataaaaact accacccgaa 754
Asn Leu Arg Xaa Leu Leu Thr Xaa Ile Lys Thr
      25                                30                                35
ggaatgaaaa aaccaaaaaa aaaaaaaaaa 783

<210> 68
<211> 996
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 140..205
<223> Von Heijne matrix
      score 5.90000009536743
      seq IILGCLALFLLLQ/RK

<221> polyA_signal
<222> 965..970

<221> polyA_site
<222> 984..996

<221> misc_feature
<222> 676..959
<223> homology
      id :AA399103
      est

<221> misc_feature
<222> 609..679
<223> homology

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id :AA399103
est

<221> misc_feature
<222> 225..433
<223> homology
id :AA398040
est

<221> misc_feature
<222> 433..563
<223> homology
id :AA398040
est

<400> 68

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aacagttacg aaggagagct gcaaaagttg cagcagaaag gttgggagtc ccgacaggtt      60
ccgtagccca cagaaaagaa gcaagggacg gcaggactgt ttcacacttt tctgcttctg      120
gaaggtgctg gacaaaaac atg gaa cta att tcc cca aca gtg att ata atc      172
                Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile
                        -20                                -15
ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat ttg cgc      220
Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg
-10                                -5                                1                                5
aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt gga ttt      268
Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe
                10                                15                                20
gak ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga atc aag      316
Xaa Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys
                25                                30                                35
gta tgt ggt cgt ggc ava cgg ggt ctc cag agg aga caa tgc ttt ctt      364
Val Cys Gly Arg Gly Xaa Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu
                40                                45                                50
ttt taaactttct ttcattgact cttaagtgcg gggctagaac acggggaaca      417
Phe
tacctgcttg cctcaaacta aaggatctag tcmtytctga aktcctctac tsacrtrtra      477
caacaatata ctgtgcaaaa ttttgcgaaa gaaatgaaat acaattgcmg cgtgcatcga      537
catttttgga agtagagatt aacyttcgt atttttactt cmtcgaagtt aagttccaaa      597
tgtgtatgtg ttaagtaaatt gttttcagta aytgggaaag ataaagtgtg atccaattta      657
agtttgtgaa aatgagtaat tccgtatcca aaytggagtt aacaccaaag tattgtacaa      717
attgcttgca cagttggtcc gtacacaata gacaggctyt gtatttttag ctgacgttgt      777
tatttgatga tgatgtactc cattttcamt acggcccgaag gagamtagta atcctccttg      837
tagtagatgt ttttgtcttg aaagtatctt ttaaagtgtt gagcacttta aggaacagac      897
ccttattaat gtyttttaag ttttattcaa tttccagtcg caaatatttt atggtatttg      957
attgtytaat aaatttgtat gatattaaaa aaaaaaaaaa      996
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<210> 69
<211> 657
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 183..338
<223> Von Heijne matrix
score 3.79999995231628
seq VMLETGGLLVSLG/QS

<221> polyA_signal
<222> 620..625

<221> polyA_site
<222> 644..657

<221> misc_feature
<222> 207..263
<223> homology
id :AA357230
est

<400> 69

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agggacttcc ggcctcgctg gcgtggacgt ttgtggtggg gcgtgttggt ccgcgctctc      60
agaactgtgc tgggaaggat ggtagggcga ctggggctca cctccgcacc gttgtaggac      120
ccggggtagg gttttgagcc cgtgggagct gccccacgcg gcctcgtcct gccaacggtc      180
gg atg gcg gag acg aag gac gca gcg cag atg ttg gtg acc ttc aag      227
  Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys
      -50          -45          -40
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg      275
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
      -35          -30          -25
gcc cag agg acc ctg tac cga gag gtg atg ctg gag acc tgt ggg ctt      323
Ala Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu
      -20          -15          -10
ctg gtt tca cta ggg caa agc att tgg ctg cat ata aca gaa aac cag      371
Leu Val Ser Leu Gly Gln Ser Ile Trp Leu His Ile Thr Glu Asn Gln
      -5          1          5          10
atc aaa ctg gct tca cct gga agg aaa ttc act aac tcg cct gat gag      419
Ile Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu
      15          20          25
aag cct gag gtg tgg ttg gct cca ggc ctg ttc ggt gcc gca gcc cag      467
Lys Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
      30          35          40
tgacgccatc aaggatgtct tggttctctg ttccttcttc ttggttcagg cttctggatt      527
gtcctcaggc tggctcctca tagggatgct ggggtgctgca gccttgactg gggcagcagg      587
cccccatggt tcaatccatc ctcccacctt ggaataaatg ctttcttttc acaatgagaa      647
aaaaaaaaaa                                     657
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<210> 70
<211> 416
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 140..205
<223> Von Heijne matrix
score 5.90000009536743
seq IILGCLALFLLLQ/RK

<221> polyA_signal
<222> 383..388

<221> polyA_site
<222> 405..416

<221> misc_feature
 <222> 225..316
 <223> homology
 id :AA398040
 est

<400> 70

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aacagttacg aaggagagct gcaaaagttg cagcagaaaag gttgggagtc ccgacaggtt      60
ccgtagccca cagaaaaagaa gcaagggacg gcaggactgt ttcacacttt tctgcttctg      120
gaaggtgctg gacaaaaaac atg gaa cta att tcc cca aca gtg att ata atc      172
                Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile
                -20                                -15

ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat ttg cgc      220
Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg
   -10                                -5                                1                                5

aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt gga ttt      268
Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe
                10                                15                                20

gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga atc aag      316
Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys
                25                                30                                35

tat gga cca ata ttt aca gtc ttt gct atg gga aac cga atg acc ttt      364
Tyr Gly Pro Ile Phe Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe
   40                                45                                50

gtt act gaa gaa gga agg aat taatgtgttt ctaaaatcca aaaaaaaaaa a      416
Val Thr Glu Glu Gly Arg Asn
   55                                60

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<210> 71
 <211> 543
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 129..176
 <223> Von Heijne matrix
 score 4.80000019073486
 seq SLFIYIFLTCSNT/SP

<221> polyA_signal
 <222> 513..518

<221> polyA_site
 <222> 530..543

<221> misc_feature
 <222> 264..500
 <223> homology
 id :AA534039
 est

<221> misc_feature
 <222> 205..315
 <223> homology
 id :T82645

est

<221> misc_feature
<222> 295..382
<223> homology
id :T82645
est

<221> misc_feature
<222> 375..405
<223> homology
id :T82645
est

<400> 71

actgtcccat	tcctccccct	acaacacaca	cacctttcag	gcagggasgn	gatgagcttc	60
cagccccaa	agtgagggt	gccacatcct	aacatasgta	tctattgaaa	aggaagcagt	120
gtgtatct	atg att ata	tct ctg ttc	atc tat ata	ttt ttg aca	tgt agc	170
	Met Ile Ile	Ser Leu Phe	Ile Tyr Ile	Phe Leu Thr	Cys Ser	
	-15		-10		-5	
aac acc tct	cca tct tat	caa gga act	caa ctc ggt	ctg ggt ctc	ccc	218
Asn Thr Ser	Pro Ser Tyr	Gln Gly Thr	Gln Leu Gly	Leu Gly Leu	Pro	
	1	5	10			
agt gcc cag	tgg tgg cct	ttg aca ggt	agg agg atg	cag tgc tgc	agg	266
Ser Ala Gln	Trp Trp Pro	Leu Thr Gly	Arg Arg Met	Gln Cys Cys	Arg	
15	20	25	30			
cta ttt tgt	ttt ttg tta	caa aac tgt	ott ttc cct	ttt ccc ctc	cac	314
Leu Phe Cys	Phe Leu Leu	Gln Asn Cys	Leu Phe Pro	Phe Pro Leu	His	
	35	40	45			
ctg att cag	cat gat ccc	tgt gag ctg	ggt ctc aca	atc tcc tgg	gac	362
Leu Ile Gln	His Asp Pro	Cys Glu Leu	Val Leu Thr	Ile Ser Trp	Asp	
	50	55	60			
tgg gct gag	gca ggg gct	tcg ctc tat	tct ccc taac	catact gtctt	ccttt	415
Trp Ala Glu	Ala Gly Ala	Ser Leu Tyr	Ser Pro			
	65	70				
cccccttgcc	acttagcagt	tatcccccca	gctatgcctt	ctccctccct	cccttgcctt	475
ggcatatatt	gtgccttatt	tatgctgcaa	atataacatt	aaactatcaa	gtgaaaaaaa	535
aaaaaaaa						543

<210> 72
<211> 605
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 285..341
<223> Von Heijne matrix
score 5.59999990463257
seq PTLCVSSSPALWA/AS

<221> polyA_signal
<222> 575..580

<221> polyA_site
<222> 592..605

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<221> misc_feature
<222> 53..296
<223> homology
      id :W07033
      est

<221> misc_feature
<222> 348..432
<223> homology
      id :W07033
      est

<221> misc_feature
<222> 435..497
<223> homology
      id :W07033
      est

<221> misc_feature
<222> 293..337
<223> homology
      id :W07033
      est

<221> misc_feature
<222> 521..560
<223> homology
      id :W07033
      est

<221> misc_feature
<222> 489..520
<223> homology
      id :W07033
      est

<221> misc_feature
<222> 15..337
<223> homology
      id :AA151004
      est

<221> misc_feature
<222> 348..412
<223> homology
      id :AA151004
      est

<221> misc_feature
<222> 434..485
<223> homology
      id :AA151004
      est

<221> misc_feature
<222> 83..324
<223> homology
      id :AA476506

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est

<221> misc_feature
<222> 347..560
<223> homology
id :AA476506
est

<221> misc_feature
<222> 16..347
<223> homology
id :W56567
est

<221> misc_feature
<222> 350..405
<223> homology
id :W56567
est

<221> misc_feature
<222> 433..470
<223> homology
id :W56567
est

<221> misc_feature
<222> 15..296
<223> homology
id :AA147584
est

<221> misc_feature
<222> 348..421
<223> homology
id :AA147584
est

<221> misc_feature
<222> 293..337
<223> homology
id :AA147584
est

<221> misc_feature
<222> 419..453
<223> homology
id :AA147584
est

<221> misc_feature
<222> 2..338
<223> homology
id :AA281959
est

<221> misc_feature
<222> 350..432

<223> homology
 id :AA281959
 est

<400> 72
 aacgcctwta agacagcgga actaagaaaa gaagaggcct gtggacagaa caatcatgtc 60
 tgactccctg gtggtgtgcg aggtagaccc agagctaaca gaaaagctga kgaaattccg 120
 cttccgaaaa gagacagaca atgcagccat cataatgaag gtggacaaa accggcagat 180
 ggtggtgctg gaggaagaat ttcagaacat tccccagag gagctcaaaa tggagttgcc 240
 ggagagacag cccagggttcg tggtttacag ctacaagtac gtgc atg acg atg gcc 296
 Met Thr Met Ala
 gag tgt cct acc ctt tgt gtt tca tct tct cca gcc ctg tgg gct gca 344
 Glu Cys Pro Thr Leu Cys Val Ser Ser Ser Pro Ala Leu Trp Ala Ala
 -15 -10 -5 1
 agc gaa aca aca gat gat gta tgc agg gag taaaaacagg ctggtgcaga 394
 Ser Glu Thr Thr Asp Asp Val Cys Arg Glu
 5 10
 cagcagagct cacaaggtg ttcgaaatcc gcaccactga tgacctcact gaggcctggc 454
 tccaagaaaa gttgtctttc tttcgttgat ctctgggctg gggactgaat tcctgatgtc 514
 tgagtcctca aggtgactgg ggacttgga cccctaggac ctgaacaacc aaggacttta 574
 aataaatttt aaaatgcaaa aaaaaaaaaa a 605

<210> 73
 <211> 864
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 136..444
 <223> Von Heijne matrix
 score 4.90000009536743
 seq VYAFLGLTAPSGS/KE

<221> polyA_signal
 <222> 835..840
 <221> polyA_site
 <222> 851..864

<221> misc_feature
 <222> 222..456
 <223> homology
 id :AA136758
 est

<221> misc_feature
 <222> 557..648
 <223> homology
 id :AA136758
 est

<221> misc_feature
 <222> 501..571
 <223> homology
 id :AA136758
 est

<221> misc_feature
<222> 130..456
<223> homology
 id :AA393612
 est

<221> misc_feature
<222> 88..130
<223> homology
 id :AA393612
 est

<221> misc_feature
<222> 501..538
<223> homology
 id :AA393612
 est

<221> misc_feature
<222> 130..458
<223> homology
 id :R59039
 est

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ggattccagc cattgctgca gctgctccac agcccttttc aggacccaaa caaccgcagc 120
cgctgttccc caggr atg gtg atc cgt gta tat att gca tct tcc tct ggc 171
Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly
-100 -95
tct aca gcg att aag aag aaa caa caa gat gtg ctt ggt ttc cta gaa 219
Ser Thr Ala Ile Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu
-90 -85 -80
gcc aac aaa ata gga ttt gaa gaa aaa gat att gca gcc aat gaa gag 267
Ala Asn Lys Ile Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu
-75 -70 -65 -60
aat cgg aag tgg atg aga gaa aat gta cct gaa aat agt cga cca gcc 315

Asn	Arg	Lys	Trp	Met	Arg	Glu	Asn	Val	Pro	Glu	Asn	Ser	Arg	Pro	Ala		
				-55					-50					-45			
aca	ggt	aac	ccc	ctg	cca	cct	cag	att	ttc	aat	gaa	agc	cag	tat	cgc	363	
Thr	Gly	Asn	Pro	Leu	Pro	Pro	Gln	Ile	Phe	Asn	Glu	Ser	Gln	Tyr	Arg		
			-40				-35						-30				
ggg	gac	tat	gat	gcc	ttc	ttt	gaa	gcc	aga	gaa	aat	aat	gca	gtg	tat	411	
Gly	Asp	Tyr	Asp	Ala	Phe	Phe	Glu	Ala	Arg	Glu	Asn	Asn	Ala	Val	Tyr		
		-25					-20					-15					
gcc	ttc	tta	ggc	ttg	aca	gcc	cca	tct	ggg	tca	aag	gaa	gca	gga	agg	459	
Ala	Phe	Leu	Gly	Leu	Thr	Ala	Pro	Ser	Gly	Ser	Lys	Glu	Ala	Gly	Arg		
	-10					-5					1				5		
tgc	aag	caa	agc	agc	aag	cca	tgaac	cttga	gcact	gtgct	ttaag	catc				510	
Cys	Lys	Gln	Ser	Ser	Lys	Pro											
				10													
ctg	aaaaatg	agt	ctccatt	gct	tttataa	aat	agcagaa	ttag	ctttgc	stt	caaaaaga					570	
aat	aggstta	atg	ttgaaat	aat	agattag	ttg	gggttttc	acat	gcaaac	amt	caaaaatg					630	
aata	caaaaat	taaa	atttga	acatt	atggt	gatt	atggtg	agg	agaatgg	gat	attaaca					690	
taaa	attata	tta	ataagta	gat	atygtag	aaat	agtgtt	gtt	acctgcc	aag	ccatcct					750	
gtata	cacca	atg	attttac	aa	agaaaaca	cc	ttccctc	ctt	ytgccat	tam	tatggca					810	
ac	taagtgt	aty	gcagct	tt	acattaaa	aag	gagaaag	ag	aaaaaaaa	aaaa						864	

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<221> polyA_site
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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<223> homology
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<221> misc_feature
<222> 788..940
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cctgaagtga cagcggagag aaccaggcag cccagaaaacc ccaggcgtgg agattgatcc 120
tgcgagagaa gggggttcat catggcggat gacctaaagc gattcttgta taaaaagtta 180
ccaagtgttg aagggtcc atg cca ttg ttg tgt cag ata gag atg gag tac 232
Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr
-75 -70
ctg tta tta aag tgg caa atg aca atg ctc cag agc atg ctt tgc gac 280
Leu Leu Leu Lys Trp Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp
-65 -60 -55 -50
ctg gtt tct tat cca ctt ttg ccc ttg caa cag acc aag gaa gca aac 328
Leu Val Ser Tyr Pro Leu Leu Pro Leu Gln Thr Lys Glu Ala Asn
-45 -40 -35
ttg gac ttt cca aaa ata aaa gta tca tct gtt act ata aca cct acc 376

Leu	Asp	Phe	Pro	Lys	Ile	Lys	Val	Ser	Ser	Val	Thr	Ile	Thr	Pro	Thr	
			-30					-25					-20			
agg	tgg	ttc	aat	tta	atc	gtt	tac	ctt	tgg	gtg	gtg	agt	ttc	ata	gcc	424
Arg	Trp	Phe	Asn	Leu	Ile	Val	Tyr	Leu	Trp	Val	Val	Ser	Phe	Ile	Ala	
		-15				-10						-5				
agc	agc	agt	gcc	aat	aca	gga	cta	att	gtc	agc	cta	gaa	aag	gaa	ctt	472
Ser	Ser	Ser	Ala	Asn	Thr	Gly	Leu	Ile	Val	Ser	Leu	Glu	Lys	Glu	Leu	
1				5				10						15		
gct	cca	ttg	ttt	gaa	gaa	ctg	aga	caa	gtt	gtg	gaa	gtt	tct			514
Ala	Pro	Leu	Phe	Glu	Glu	Leu	Arg	Gln	Val	Val	Glu	Val	Ser			
			20					25								
taatctgaca	gtggttttcag	tgtgtacctt	atcttcatta	taacaacaca	atatcaatcc											574
agcaatcttt	agactacaat	aatactttta	tccatgtgct	caagaaagg	cccctttttc											634
caacttatac	taaagagcta	gcatatagat	gtaatttata	gatagatcag	ttgctatatt											694
ttctggtgta	gggtctttct	tatttagtga	gatctaggga	taccacagaa	atggttcagt											754
ctatcaacag	ctcccatgga	gtagtctgg	tcacagatat	ggatgagaga	ttytattcag											814
tggatcagaa	tcaaactggt	acattgatcc	acttgagccg	ttaagtgtctg	ccaattgtac											874
aatatgccca	ggcttgacga	ataaagccaa	ctttttattg	tgaataataa	taaggacata											934
tttttyttca	gattatgttt	tatttytttg	cattgagtga	ggaacataaa	atggcttggt											994
aaaagtaata	aatcagtag	aatcactaaa	aaaaaaaaa													1033

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 <222> 490..499

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tgacacc	atg	aag	cct	gtg	ctg	cct	ctc	cag	ttc	ctg	gtg	gtg	ttc	tgc		109
	Met	Lys	Pro	Val	Leu	Pro	Leu	Gln	Phe	Leu	Val	Val	Phe	Cys		
		-20						-15					-10			
cta	gca	ctg	cag	ctg	gtg	cct	ggg	agt	ccc	aag	cag	cg	gtt	ctg	aag	157
Leu	Ala	Leu	Gln	Leu	Val	Pro	Gly	Ser	Pro	Lys	Gln	Arg	Val	Leu	Lys	
		-5				1					5					
tat	atc	ttg	gaa	cct	cca	ccc	tgc	ata	tca	gca	cct	gaa	aac	tgt	act	205
Tyr	Ile	Leu	Glu	Pro	Pro	Pro	Cys	Ile	Ser	Ala	Pro	Glu	Asn	Cys	Thr	
10				15				20								
cac	ctg	tgt	aca	atg	cag	gaa	gat	tgc	gag	aaa	gga	ttt	cag	tgc	tgt	253
His	Leu	Cys	Thr	Met	Gln	Glu	Asp	Cys	Glu	Lys	Gly	Phe	Gln	Cys	Cys	
25				30				35					40			
tcc	tcc	ttc	tgt	ggg	ata	gtc	tgt	tca	tca	gaa	aca	ttt	caa	aag	cgc	301
Ser	Ser	Phe	Cys	Gly	Ile	Val	Cys	Ser	Ser	Glu	Thr	Phe	Gln	Lys	Arg	
			45					50					55			
aac	aga	atc	aaa	cac	aag	ggc	tca	gaa	gtc	atc	atg	cct	gcc	aac		346

Asn Arg Ile Lys His Lys Gly Ser Glu Val Ile Met Pro Ala Asn	
60 65 70	
tgaggcatat ttcctagatc attttgcctc tacgatgttt tttcttggtc cacctttagg	406
aaggatttga gaagcaagaa actggaggcc caatatctaa cctgcaaadc gtttttgagt	466
ttggcaataa aggctaactc accaaaaaaaa aaa	499

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<221> misc_feature
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id :HUM00TW170
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<221> misc_feature

<222> 805..861
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<221> misc_feature
 <222> 542..595
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<221> misc_feature
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taatgttaag aatgggtcag aaatggggct gctcagcctc tggaccaacc ccaggaagag      180
tctgaagagc agccagtgtt tcggcttgtg ccctgtatac ttgaagctgc caaacaagta      240
cgttctgaaa atccagaatg gcttcatggtt tac atg cac att tta caa ctg ctt      294
                                   Met His Ile Leu Gln Leu Leu
                                   -40
act aca gtg gat gat gga att caa gca att gta cat tgt cct gac act      342
Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His Cys Pro Asp Thr
-35                                -30                                -25                                -20
gga aaa gac att tgg aat tta ctt ttt gac ctg gtc tgc cat gaa ttc      390
Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val Cys His Glu Phe
-15                                -10                                -5
tgc cag tct gat gat cca gcc atc att ctt caa gaa cag aaa aca gtg      438
Cys Gln Ser Asp Asp Pro Ala Ile Ile Leu Gln Glu Gln Lys Thr Val
1                                5                                10
cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat gcc tca cag act      486
Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr Ala Ser Gln Thr
15                                20                                25
gag caa gag tat cta aag ata gaa aaa gta gat ctt cct cta att gac      534
Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val Asp Leu Pro Leu Ile Asp
30                                35                                40                                45
agc ctc att cgg gtc tta caa aat atg gaa cag tgt cag aaa aaa cca      582
Ser Leu Ile Arg Val Leu Gln Asn Met Glu Gln Cys Gln Lys Lys Pro
50                                55                                60
gag aac tcg gca gga gtc taacacagag gaaactaaaa ggactgattt      630
Glu Asn Ser Ala Gly Val
65

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aacccaagat	gatttccact	tgaaaatctt	aaaaggatat	tgttatgggtg	aagtttctgt	690
ctaataattt	ttcaggcatt	aacaaaggag	acggtggctc	agggagtaaa	ggaaggccgt	750
tgagcaaaca	gaagtgttcc	tctgcaattt	caaaarcctt	cttctttcta	tagcccctgt	810
gggtggaaga	ttttattaaa	atcctacgtg	aagttgataa	ggcgcttgct	kgatgacttg	870
gaaaaaaamc	ttcccaagtt	tgaaggttca	gaastaaaaa	rscktgaatg	ggaattactt	930
sstgtbcaag	aaaataaact	ttatTTTTct	cactgaaaaa	aaaaaaaa		978

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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
 <222> 136..193

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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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 <222> 387..400

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gctcctctcc	acctctagcc	tgctcatttc	cagctcagaa	attctactaa	tggcgttttt	180
tcttctgtaa	aaaggaa	atg aac	agg gtc	cct gct	gat tct cca	230
		Met Asn Arg Val	Pro Ala Asp	Ser Pro Asn	Met	
		-25		-20		
tgt cta atc	tgt tta ctg	agt tac	ata gca	ctt gga	gcc atc cat	278
Cys Leu Ile	Cys Leu Leu	Ser Tyr Ile	Ala Leu Gly	Ala Ile His	Ala	
-15		-10		-5		
aaa atc tgt	aga aga gca	ttc cag	gaa gag	gga aga	gca aat gca	326
Lys Ile Cys	Arg Arg Ala	Phe Gln Glu	Glu Gly Arg	Ala Asn Ala	Lys	
1	5	10	15			
acg ggc	gtg aga gct	tgg tgc	ata cag	cca tgg	gcc aaa	375
Thr Gly Val	Arg Ala Trp	Cys Ile Gln	Pro Trp	Ala Lys		
	20	25				
ttggaatagc	caaaaaaaaa	aaaaa				400

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<220>

<221> sig_peptide
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<221> polyA_site
 <222> 1154..1166

<221> misc_feature
 <222> 22..377
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<221> misc_feature
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 <223> homology

id :AA306911
est

<221> misc_feature
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id :AA306911
est

<221> misc_feature
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<223> homology
id :AA417777
. est

<221> misc_feature
<222> 10..447
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id :AA236327
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id :AA410332
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id :N32991
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature


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Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu Leu Leu Ser
                                -15      -10      -5
tat gac ctc ttt gtc aat tcc ttc tca gaa ctg ctc caa aag act cct      271
Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln Lys Thr Pro
                                1      5      10
gtc atc cag ctt gtg ctc ttc atc atc cag gat att gca gtc ctc ttc      319
Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala Val Leu Phe
                                15      20      25      30
aac atc atc atc att ttc ctc atg ttc ttc aac acc tcc gtc ttc cag      367
Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Ser Val Phe Gln
                                35      40      45
gct ggc ctg gtc aac ctc cta ttc cat aag ttc aaa ggg acc atc atc      415
Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly Thr Ile Ile
                                50      55      60
ctg aca gct gtg tac ttt gcc ctc agc atc tcc ctt cat gtc tgg gtc      463
Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His Val Trp Val
                                65      70      75
atg aac tta cgc tgg aaa aac tcc aac agc ttc ata tgg aca gat gga      511
Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp Thr Asp Gly
                                80      85      90
ctt caa atg ctg ttt gta ttc cag aga cta gca gca gtg ttg tac tgc      559
Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val Leu Tyr Cys
                                95      100      105      110
tac ttc tat aaa cgg aca gcc gta aga cta ggc gat cct cac ttc tac      607
Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro His Phe Tyr
                                115      120      125
cag gac tct ttg tgg ctg cgc aag gag ttc atg caa gtt cga agg      652
Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val Arg Arg
                                130      135      140
tgacctcttg tcacactgat ggatactttt ccttcctgat agaagccaca tttgctgctt      712
tgcaggggaga gttggcccta tgcattgggca aacagctgga ctttccaagg aagggttcaga      772
ctagctgtgt tcagcattca agaaggaaga tccccctct tgcacaatta gagtgtcccc      832
atcggtctcc agtgcgcat ccttccttg ccttctacct ctgttccacc ccttccttc      892
ctctcctctc tgtaccattc attctccctg accggccttt cttgccgagg gttctgtggc      952
tcttaccctt gtgaagcttt tccttttagcc tgggacagaa ggacctcccg gcccccaaag      1012
gatctcccag wtgaccaaag gatgcgaaga gtgatagtta cgntgctcct gactgatcac      1072
accgcagaca tttagatttt tataccaag gcactttaaa aaaatgtttt ataaatagag      1132
aataaattga attyttgttc caaaaaaaaaa aaaa      1166

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<210> 80
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 <213> Homo sapiens

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 <223> Von Heijne matrix
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 seq LPFSLVSMMLVTQG/LV

<221> polyA_signal
 <222> 722..727

<221> polyA_site

<222> 743..754

<221> misc_feature

<222> 116..450

<223> homology

id :W68799

est

<221> misc_feature

<222> 593..710

<223> homology

id :W68799

est

<221> misc_feature

<222> 18..117

<223> homology

id :W68799

est

<221> misc_feature

<222> 561..598

<223> homology

id :W68799

est

<221> misc_feature

<222> 48..511

<223> homology

id :AA149518

est

<221> misc_feature

<222> 593..673

<223> homology

id :AA149518

est

<221> misc_feature

<222> 535..710

<223> homology

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<222> 256..405

<223> homology

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est

<221> misc_feature

<222> 432..511

<223> homology

id :W80356

est

<221> misc_feature

<222> 392..437


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    est

<221> misc_feature
<222> 535..710
<223> homology
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    est

<221> misc_feature
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<223> homology
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<221> misc_feature
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<221> misc_feature
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<221> misc_feature
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<223> homology
    id :AA142865
    est

<221> misc_feature
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<223> homology
    id :AA405876
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<221> misc_feature
<222> 21..271
<223> homology
    id :AA405876
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<221> misc_feature
<222> 121..450
<223> homology
    id :W68728
    est

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<221> misc_feature
 <222> 592..710
 <223> homology
 id :W68728
 est

<400> 80

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ggcctgctgg gcttggcaac gagggactcg gcctcggagg cgacccagac cacacagaca      120
ctgggtcaag gagtaagcag aggataaaca actggaagga gagcaagcac aaagtcatac      179
atg gct tca gcg tct gct cgt gga aac caa gat aaa gat gcc cat ttt      227
Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
      -65                      -60                      -55
cca cca cca agc aag cag agc ctg ttg ttt tgt cca aaa tca aaa ctg      275
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
      -50                      -45                      -40
cac atc cac aga gca gag atc tca aag att atg cga gaa tgt cag gaa      323
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
      -35                      -30                      -25
gaa agt ttc tgg aag aga gct ctg cct ttt tct ctt gta agc atg ctt      371
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
      -20                      -15                      -10                      -5
gtc acc cag gga cta gtc tac caa ggt tat ttg gca gct aat tct aga      419
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
      1                      5                      10
ttt gga tca ttg ccc aaa gtt gca ctt gct ggt ctc ttg gga ttt ggc      467
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
      15                      20                      25
ctt gga aag gta tca tac ata gga gta tgc cag agt aaa ttc cat ttt      515
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
      30                      35                      40
ttt gaa gat cag ctc cgt ggg gct ggt ttt ggt ccw aca gca      557
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Thr Ala
      45                      50                      55
taacaggcac tgcctcctta cctgtgagga atgcaaaata aagcatggat taagtgagaa      617
gggagactct cagccttcag cttcctaaat tctgtgtctg tgactttcga agttttttaa      677
acctctgaat ttgtacacat ttaaaatttc aaggtgtact ttaaaatnaa aatacttcta      737
atgtvaaaaa aaaaaaa      754

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<210> 81
 <211> 709
 <212> DNA
 <213> Homo sapiens

<220>

<221> sig_peptide
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<221> polyA_signal
 <222> 680..685

<221> polyA_site
 <222> 697..708

<221> misc_feature
<222> 137..291
<223> homology
id :AA121372
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<221> misc_feature
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id :AA121372
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<221> misc_feature
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<221> misc_feature
<222> 460..501
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<221> misc_feature
<222> 432..465
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est

<221> misc_feature
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<223> homology
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<221> misc_feature
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<223> homology
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<221> misc_feature
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<223> homology
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est

<221> misc_feature
<222> 358..670
<223> homology
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<221> misc_feature
<222> 312..344
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est

<221> misc_feature
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<223> homology
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est

<221> misc_feature
<222> 150..258
<223> homology
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<221> misc_feature
<222> 95..171
<223> homology
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<221> misc_feature
<222> 322..628
<223> homology
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<221> misc_feature
<222> 445..670
<223> homology
id :AA454502
est

<221> misc_feature
<222> 2..102
<223> homology
id :R09314
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<221> misc_feature
<222> 95..171
<223> homology
id :R09314
est

<221> misc_feature
<222> 150..222

<223> homology
 id :R09314
 est

<400> 81

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ggcgggagaag	ggtgcgggct	cttcgccctt	tgtgtccttc	tttcactaac	ttctggactt	120
tccagctctt	ccgaagtctg	ttcttgcgca	aagcccaaag	gctggaaaac	cgcccaag	178
atg acc agc atg act cag tct ctg cgg gag gtg ata aag gcc atg acc						226
Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr						
-40	-35		-30		-25	
aag gct cgc aat ttt gag aga gtt ttg gga aag att act ctt gtc tct						274
Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser						
	-20		-15		-10	
gct gct cct ggg aaa gtg att tgt gaa atg aaa gta gaa gaa gag cat						322
Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu Glu His						
	-5		1		5	
acc aat gca ata ggc act ctc cac ggc ggt ttg aca gcc acg tta gta						370
Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val						
10	15		20			
gat aac ata tca aca atg gct ctg cta tgc acg gaa agg gga gca ccc						418
Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro						
25	30		35		40	
gga gtc agt gtc gat atg aac ata acg tac atg tca cct gca aaa tta						466
Gly Val Ser Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu						
	45		50		55	
gga gag gat ata gtg att aca gca cat gtt ctg aag caa gga aaa aca						514
Gly Glu Asp Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr						
	60		65		70	
ctt gca ttt acc tct gtg ggt ctg acc aac aag gcc aca gga aaa tta						562
Leu Ala Phe Thr Ser Val Gly Leu Thr Asn Lys Ala Thr Gly Lys Leu						
	75		80		85	
ata gca caa gga aga cac aca aaa cac ctg gga aac tgagagaaca						608
Ile Ala Gln Gly Arg His Thr Lys His Leu Gly Asn						
	90		95		100	
gcagaatgac ctaaagaaac ccaacaatga atatcaagta tagatttgac tcaaacaatt						668
gtaattttttg aaataaacta gcaaaaccaa aaaaaaaaaa g						709

<210> 82

<211> 243

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 100..171

<223> Von Heijne matrix

score 3.70000004768372

seq ILFNLLIFLCGFT/NY

<221> polyA_signal

<222> 211..216

<221> polyA_site

<222> 230..243

<221> misc_feature

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<222> 2..164
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<221> misc_feature
<222> 2..164
<223> homology
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      est

<221> misc_feature
<222> 5..164
<223> homology
      id :AA224847
      est

<221> misc_feature
<222> 10..164
<223> homology
      id :AA161042
      est

<221> misc_feature
<222> 2..84
<223> homology
      id :AA088770
      est

<221> misc_feature
<222> 104..164
<223> homology
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      est

<221> misc_feature
<222> 10..164
<223> homology
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<221> misc_feature
<222> 79..164
<223> homology
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<221> misc_feature
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<221> misc_feature
<222> 109..164
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<221> misc_feature
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<223> homology
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<221> misc_feature
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<223> homology
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<221> misc_feature
<222> 200..229
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id :AA601071
est

<221> misc_feature
<222> 200..229
<223> homology

id :AA225190
est

<400> 82

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ttcagaactc actgccaaga gccctgaaca ggagccacc atg cag tgc ttc agc 114
                                     Met Gln Cys Phe Ser
                                     -20
ttc att aag acc atg atg atc ctc ttc aat ttg ctc atc ttt ctg tgt 162
Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe Leu Cys
      -15      -10      -5
ggc ttc acc aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg 210
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met
      1      5      10
cat aaa cct gtt aca atg taaaaaaaaa aaaaa 243
His Lys Pro Val Thr Met
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<210> 83

<211> 829

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 346..408

<223> Von Heijne matrix

score 5.5

seq SFLPSALVIWTS/AF

<221> polyA_signal

<222> 792..797

<221> polyA_site

<222> 817..829

<221> misc_feature

<222> 260..464

<223> homology

id :H57434

est

<221> misc_feature

<222> 118..184

<223> homology

id :H57434

est

<221> misc_feature

<222> 56..113

<223> homology

id :H57434

est

<221> misc_feature

<222> 454..485

<223> homology

id :H57434
est

<221> misc_feature
<222> 118..545
<223> homology
id :N27248
est

<221> misc_feature
<222> 65..369
<223> homology
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<221> misc_feature
<222> 471..519
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<221> misc_feature
<222> 61..399
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<222> 408..452
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<222> 60..399
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<221> misc_feature
<222> 393..432
<223> homology
id :H29351
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<221> misc_feature
<222> 260..444
<223> homology
id :AA459511
est

<221> misc_feature
<222> 449..545
<223> homology
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<221> misc_feature

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<222> 117..184
<223> homology
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      est

<221> misc_feature
<222> 122..399
<223> homology
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      est

<221> misc_feature
<222> 393..434
<223> homology
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<221> misc_feature
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<223> homology
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<221> misc_feature
<222> 118..399
<223> homology
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<221> misc_feature
<222> 268..545
<223> homology
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<221> misc_feature
<222> 268..545
<223> homology
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      est

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ctcaaacggc ctagtgcttc gcgcttccgg agaaaatcag cgggtctaatt aattcctctg      180
gtttgttgaa gcagttacca agaattctca accctttccc acaaaagcta attgagtaca      240
cgttcctgtt gactacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg      300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt      357
                                     Met Trp Trp Phe
                                     -20
cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
      -15                               -10                               -5
gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata      453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
      1                               5                               10                               15
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca gaa      501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Glu

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	20	25	30	
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtc tta tgt caa				549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln				
	35	40	45	
aaa tagaaatcag gaagataatt caacttaaag aagttcattt catgaccaa				602
Lys				
ctcttcagaa acatgtcttt acaagcatat ctcttgattt gctttctaca ctgttgaatt				662
gtctggcaat atttctgcag tggaaaattt gatttagcta gttcttgact tggataaata				722
tggtaagggtg ggcttttccc cctgtgtaat tggctacsac gtcttacttg agccaagttg				782
gtaagttgaa ataaatgat watgagagtg acacavaaaa aaaaaaa				829

<210> 84
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 <212> DNA
 <213> Homo sapiens

<220>
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<221> polyA_signal
 <222> 644..649

<221> polyA_site
 <222> 663..674

<221> misc_feature
 <222> 194..592
 <223> homology
 id :AA496246
 est

<221> misc_feature
 <222> 1..100
 <223> homology
 id :AA496246
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<221> misc_feature
 <222> 99..202
 <223> homology
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<221> misc_feature
 <222> 187..592
 <223> homology
 id :AA476481
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<221> misc_feature
 <222> 594..661
 <223> homology
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est

<221> misc_feature
<222> 188..592
<223> homology
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<221> misc_feature
<222> 594..661
<223> homology
id :AA496245
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<221> misc_feature
<222> 194..444
<223> homology
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<221> misc_feature
<222> 1..102
<223> homology
id :AA476480
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<221> misc_feature
<222> 99..187
<223> homology
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<221> misc_feature
<222> 437..592
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<221> misc_feature
<222> 594..661
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<221> misc_feature
<222> 441..592
<223> homology
id :AA554685
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<221> misc_feature
<222> 594..661
<223> homology
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est

<221> misc_feature
<222> 414..503

<223> homology
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 est

<221> misc_feature

<222> 510..539

<223> homology
 id :AA215595
 est

<400> 84

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gggtgggtgg actagaagca tttgggagta gtggccaggg gccctggacg ctagccacgg      120
agctgctgca cagagcctgg tgtccacaag cttccagggt ggggttggag cctggg atg      179
                                         Met

agc ccc ggc agc gcc ttg gcc ctt ctg tgg tcc ctg cca gcc tct gac      227
Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser Asp
      -15                               -10                               -5
ctg ggc cgg tca gtc att gct gga ctc tgg cca cac act ggc gtt ctc      275
Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val Leu
      1                               5                               10
atc cac ttg gaa aca agc cag tct ttt ctg caa ggt cag ttg acc aag      323
Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr Lys
      15                               20                               25                               30
agc ata ttt ccc ctc tgt tgt aca tcg ttg ttt tgt gtt tgt gtt gta      371
Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val Val
      35                               40                               45
aca gtg ggt gga ggg agg gtg ggg tct aca ttt gtt gca tgagtcgatg      420
Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala
      50                               55
ggtcagaact ttagtatacg catgcgtcct ctgagtgaac gggcattttg tcgaaaataa      480
gcaccttggt aactaaaccc ctctaatagc tataaaggct ttagttctgt attgattaag      540
ttactgtaaa agcttgggtt tatttttgta ggacttaatg gctaagaatt agggaacata      600
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ttaaaaaaaaaaaaaa

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<210> 85

<211> 478

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 179..319

<223> Von Heijne matrix
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<221> polyA_signal

<222> 461..466

<221> polyA_site

<222> 465..478

<221> misc_feature

<222> 2..464

<223> homology

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<221> misc_feature
<222> 8..464
<223> homology
id :AA312901
est

<221> misc_feature
<222> 2..416
<223> homology
id :AA401411
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<221> misc_feature
<222> 2..349
<223> homology
id :R64030
est

<221> misc_feature
<222> 56..464
<223> homology
id :AA400108
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<221> misc_feature
<222> 126..273
<223> homology
id :AA010825
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<221> misc_feature
<222> 2..147
<223> homology
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<221> misc_feature
<222> 358..435
<223> homology
id :AA010825
est

<221> misc_feature
<222> 78..464
<223> homology
id :AA504732
est

<221> misc_feature
<222> 90..441
<223> homology
id :H60506
est

<221> misc_feature

<222> 59..349
<223> homology
id :AA346780
est

<221> misc_feature
<222> 2..331
<223> homology
id :AA281167
est

<221> misc_feature
<222> 6..236
<223> homology
id :R35805
est

<221> misc_feature
<222> 232..284
<223> homology
id :R35805
est

<221> misc_feature
<222> 41..307
<223> homology
id :H13784
est

<221> misc_feature
<222> 2..40
<223> homology
id :H13784
est

<221> misc_feature
<222> 64..280
<223> homology
id :AA128122
est

<221> misc_feature
<222> 293..349
<223> homology
id :AA128122
est

<221> misc_feature
<222> 332..385
<223> homology
id :AA128122
est

<221> misc_feature
<222> 163..420
<223> homology
id :AA555127
est

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<400> 85
aagtccttcg cgccctcctc gccctcccca ccgacatcat gctccagttc ctgcttggat      60
ttacactggg caacgtgggt ggaatgtatc tggctcagaa ctatgatata ccaaacctgg      120
ctaaaaaact tgaagaaatt aaaaaggact tggatgccaa gaagaaaccc cctagtgc      178
atg aga ctg cct cca gca ctg cct tca gga tat act gat tct act gct      226
Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser Thr Ala
      -45      -40      -35
ctt gag ggc ctc gtt tac tat ctg aac caa aag ctt ttg ttt tcg tct      274
Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe Ser Ser
      -30      -25      -20
cca gcc tca gca ctt ctc ttc ttt gct aga ccc tgt gtt ttt tgc ttt      322
Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe Cys Phe
      -15      -10      -5      1
aaa gca agc aaa atg ggg ccc caa ttt gag aac tac cca aca ttt cca      370
Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr Phe Pro
      5      10      15
aca tac tca cct ctt ccc ata atc cct ttc caa ctg cat ggg agg ttc      418
Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly Arg Phe
      20      25      30
taagactgga attatggtgc tagattagta aacatgactt ttaatgaaaa aaaaacaaaa      478

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<210> 86
<211> 952
<212> DNA
<213> Homo sapiens

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<220>
<221> sig_peptide
<222> 112..237
<223> Von Heijne matrix
      score 7.19999980926514
      seq ILFSLSFLLVIIT/FP

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<221> polyA_signal
<222> 910..915

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<221> polyA_site
<222> 940..952

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<400> 86
aatactttct cctctcccct ctccaagca catctgagtt gctgcctgtt cttcacactt      60
agctccaaac ccatgaaaaa ttgccaagta taaaagcttc tcaagaatga g atg gat      117
                               Met Asp
tct agg gtg tct tca cct gag aag caa gat aaa gag aat ttc gtg ggt      165
Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe Val Gly
      -40      -35      -30      -25
gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg atc ctg ttt tcc ctc      213
Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe Ser Leu
      -20      -15      -10
tct ttc ctg ttg gtg atc att acc ttc ccc atc tcc ata tgg atg tgc      261
Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp Met Cys
      -5      1      5
ttg aag att tgatcctggt cctgccatgc ataratgtgt ttgtcaaagt      310
Leu Lys Ile
      10
tgacctccga acagttactt gcaacattcc tccacaagag atcctcacca rgagactccg      370

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taactactca ggtagatgga gttgtctatt acagaatcta tagtgctgtc tcagcagtgg 430
ctaakgtcaa cgatgtccat caagcaacat ttctgctggc tcaaaccact ctgagaaatg 490
tcktagggac acaggacctt gtccccagat cttaggctgg acgagaagag atcgcccata 550
agcatccaga ctkttacttga tgatgccacc gaactgggtg gggatccggg tggcccgagt 610
ggaaatcaaa gatgttcgga ttcccggtgca gttgcagaga tccatggcag ccgaggstga 670
ggccaccggg gaagsgagag ccaaggtcct tgcagctgaa ggagaaatga atgsttccaa 730
atccctgaag tcagcctcca tggtgstggs tgagtytccc atagctytcc agstgsgsta 790
cctgcagacc ttgagcacgg tagccaccga gaagaatttt acgattgtgt ttctbtgcc 850
catgaatata ctagagggca ttggtggcgt cagstatgat aaccacaaga agsttbscaa 910
ataaagcctg aggtcybctt gcggtagtca aaaaaaaaaa aa 952

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<210> 87
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

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<400> 87
Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu
      -10                      -5                      1
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
      5                      10                      15
Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
      20                      25                      30                      35
Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
      40                      45                      50
Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
      55                      60                      65
Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys
      70                      75                      80
Lys Thr Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg
      85                      90                      95
Gly Arg Ala Gln Trp Asp Ser Leu Cys Gly Arg Cys Ile Gln Arg Asp
      100                      105                      110                      115
Tyr Leu Lys

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<210> 88
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35..-1

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<400> 88
Met Leu Thr Val Asn Asp Val Arg Phe Tyr Arg Asn Val Arg Ser Asn
-35                      -30                      -25                      -20
His Phe Pro Phe Val Arg Leu Cys Gly Leu Leu His Leu Trp Leu Lys
      -15                      -10                      -5
Val Phe Ser Leu Lys Gln Leu Lys Lys Ser Trp Ser Lys Tyr Leu
      1                      5                      10
Phe Glu Ser Cys Cys Tyr Arg Ser Leu Tyr Val Cys Val Phe Ile

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15

20

25

<210> 89
 <211> 163
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 89

Met	Ser	Pro	Ala	Phe	Arg	Ala	Met	Asp	Val	Glu	Pro	Arg	Ala	Lys	Gly
-30						-25					-20				
Ser	Phe	Trp	Ser	Pro	Leu	Ser	Thr	Arg	Ser	Gly	Gly	Thr	His	Ala	Cys
-15					-10					-5					1
Ser	Ala	Ser	Met	Arg	Gln	Pro	Trp	Ala	Ser	Pro	Trp	Ser	Gln	Gly	Asn
		5						10					15		
Ile	Ser	Ser	Thr	Arg	Pro	Ser	Leu	Leu	Arg	Cys	Ala	Asn	Ser	Leu	Pro
	20						25					30			
Ser	Thr	Lys	Asp	Lys	Ala	Lys	Gly	Pro	Leu	Leu	Ala	Gly	His	Pro	Cys
	35					40					45				
Pro	Ile	Phe	Ser	Pro	Gly	Pro	Phe	Pro	Cys	Gly	His	Arg	Glu	Val	Trp
50					55					60					65
Pro	Glu	Tyr	Pro	Thr	Pro	Ala	Pro	Leu	His	Pro	Glu	Leu	Gly	Ala	Thr
				70					75					80	
Ser	Glu	Val	Ser	Ser	Leu	Ser	Glu	His	Xaa	Phe	Pro	Cys	Ser	Ser	Arg
			85					90					95		
Gly	Leu	Ser	Arg	Leu	Ser	Asp	Ala	Gly	Ala	Xaa	Xaa	Pro	Glu	Xaa	Lys
			100				105					110			
Gly	Val	Gln	Pro	Val	Val	Cys	Lys	Ala	Leu	Xaa	Gly	Thr	Ala	Glu	Thr
	115					120					125				
Pro	Pro	Pro													
130															

<210> 90
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 90

Met	Leu	Gly	Thr	Thr	Gly	Leu	Gly	Thr	Gln	Gly	Pro	Ser	Gln	Gln	Ala
-30						-25					-20				
Leu	Gly	Phe	Phe	Ser	Phe	Met	Leu	Leu	Gly	Met	Gly	Gly	Cys	Leu	Pro
-15						-10					-5				
Gly	Phe	Leu	Leu	Gln	Pro	Pro	Asn	Arg	Ser	Pro	Thr	Leu	Pro	Ala	Ser
1				5					10					15	
Thr	Phe	Ala	His												
			20												

<210> 91

[illegible][illegible][illegible]

<211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 95
 Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
 -15 -10 -5
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Gly Lys Met
 1 5 10 15
 Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
 Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
 35 40 45
 Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
 50 55 60
 Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
 65 70

<210> 96
 <211> 172
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 96
 Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
 -20 -15 -10
 Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
 -5 1 5 10
 Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
 15 20 25
 Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
 30 35 40
 Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala
 45 50 55
 Leu Ser Pro Glu Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu
 60 65 70 75
 Val Leu Gly Ile Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe
 80 85 90
 Gln Glu Asn Asn Pro Phe Cys Cys Thr Cys Lys Trp Ser Cys Ala Tyr
 95 100 105
 Leu Trp Tyr Gly Leu Ile Ile Tyr Val Cys Ser Asp His Pro Phe Leu
 110 115 120
 Pro Lys Cys Ser Pro Lys Ser Asn Gly Lys Thr Ser Leu Leu Asp Gln
 125 130 135
 Thr Val Val Gly Tyr Leu Val Trp Ser Lys Cys Thr
 140 145 150

<210> 97
 <211> 56
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

<400> 97
 Met Cys Phe Pro Glu His Arg Arg Gln Met Tyr Ile Gln Asp Arg Leu
 -40 -35 -30
 Asp Ser Val Thr Arg Arg Ala Arg Gln Gly Arg Ile Cys Ala Ile Leu
 -25 -20 -15
 Leu Leu Gln Ser Gln Cys Ala Tyr Trp Ala Leu Pro Glu Pro Arg Thr
 -10 -5 1 5
 Leu Asp Gly Gly His Leu Met Gln
 10

<210> 98
 <211> 46
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 98
 Met Gln Asn His Leu Gln Thr Arg Pro Leu Phe Leu Thr Cys Leu Phe
 -20 -15 -10
 Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu Cys Leu Ile
 -5 1 5 10
 Leu Gln Cys Ser Val Phe Ser Phe Ala Phe Phe Ala Leu Trp
 15 20

<210> 99
 <211> 251
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 99
 Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro
 -25 -20 -15
 Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr
 -10 -5 1
 Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro
 5 10 15 20
 Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys Val Arg Arg
 25 30 35
 Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr

-30 -25 -20
 Ala Leu Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro
 -15 -10 -5 1
 Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser
 5 10 15
 Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser
 20 25 30
 Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp
 35 40 45
 Leu
 50

<210> 102
 <211> 126
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 102
 Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu Leu Thr
 -20 -15 -10 -5
 Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp His Gly
 1 5 10
 Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu Glu Pro
 15 20 25
 Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys Tyr Tyr Ile
 30 35 40
 Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser Phe Phe
 45 50 55 60
 Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu Arg Lys Val
 65 70 75
 Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val Ser His Leu
 80 85 90
 Arg Tyr Phe Gly Ser Ser Arg Gly Lys Ala Phe Ser Leu Thr
 95 100 105

<210> 103
 <211> 273
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -45..-1

<400> 103
 Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
 -45 -40 -35 -30
 Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
 -25 -20 -15
 Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
 -10 -5 1
 Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys

5					10					15						
Phe	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln	
20					25					30					35	
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala	
				40						45				50		
Tyr	Arg	Glu	Val	Gln	Glu	Lys	Arg	His	Arg	Glu	Ala	His	Gly	Glu	Asn	
			55					60					65			
Ser	Gly	Arg	Leu	Tyr	Leu	Asn	Pro	Gly	Lys	Lys	Arg	Gly	Gly	Leu	Trp	
		70				75					80					
Trp	Thr	Tyr	Val	Cys	Ser	Leu	Val	Phe	Lys	Ala	Ser	Val	Asp	Ile	Ala	
	85					90				95						
Phe	Leu	Tyr	Val	Phe	His	Ser	Phe	Tyr	Pro	Lys	Tyr	Ile	Leu	Pro	Pro	
100					105					110					115	
Val	Val	Lys	Cys	His	Ala	Asp	Pro	Cys	Pro	Asn	Ile	Val	Asp	Cys	Phe	
				120					125					130		
Ile	Ser	Lys	Pro	Ser	Glu	Lys	Asn	Ile	Phe	Thr	Leu	Phe	Met	Val	Ala	
			135					140					145			
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu	Ile	Tyr	Leu	
		150				155						160				
Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys	Ala	Gln	Ala	
	165					170					175					
Met	Xaa	Thr	Gly	His	His	Pro	Xaa	Asp	Thr	Thr	Phe	Ser	Xaa	Lys	Gln	
180					185					190					195	
Xaa	Asp	Xaa	Xaa	Ser	Gly	Asp	Xaa	Ile	Phe	Leu	Gly	Ser	Asp	Ser	His	
				200					205					210		
Xaa	Pro	Xaa	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys	Lys	Thr	Ile	
			215					220					225			
Leu																

<210> 104

<211> 158

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37..-1

<400> 104

Met	Ala	Ser	Lys	Ile	Leu	Leu	Asn	Val	Gln	Glu	Glu	Val	Thr	Cys	Pro
	-35						-30					-25			
Ile	Cys	Leu	Glu	Leu	Leu	Thr	Glu	Pro	Leu	Ser	Leu	Asp	Cys	Gly	His
	-20					-15					-10				
Ser	Leu	Cys	Arg	Ala	Cys	Ile	Thr	Val	Ser	Asn	Lys	Glu	Ala	Val	Thr
-5					1			5						10	
Ser	Met	Gly	Gly	Lys	Ser	Ser	Cys	Pro	Val	Cys	Gly	Ile	Ser	Tyr	Ser
		15					20					25			
Phe	Glu	His	Leu	Gln	Ala	Asn	Gln	His	Arg	Ala	Asn	Ile	Val	Glu	Arg
	30					35					40				
Leu	Lys	Glu	Val	Lys	Leu	Ser	Pro	Asp	Asn	Gly	Lys	Lys	Arg	Asp	Leu
	45					50				55					
Cys	Asp	His	His	Gly	Glu	Lys	Leu	Leu	Leu	Phe	Cys	Lys	Glu	Asp	Arg
60					65					70				75	
Lys	Val	Ile	Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	Glu	His	Arg	Gly	His
			80					85					90		
His	Thr	Gly	Pro	His	Gly	Gly	Ser	Ile	Gln	Gly	Met	Ser	Gly	Glu	Thr
			95					100					105		

Pro Gly Ser Pro Gln Glu Ala Glu Glu Gly Arg Gly Gly Ser
 110 115 120

<210> 105
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 105
 Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
 -15 -10 -5
 Val His Thr Thr Leu Ser Lys Ser Asp Ala Xaa Lys Pro Pro Gln Arg
 1 5 10
 Arg Cys Trp Arg Arg Val Ser Phe Gln Ile Ser Arg Cys Lys Thr Gly
 15 20 25
 Val Trp Trp
 30

<210> 106
 <211> 359
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34..-1

<400> 106
 Met Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr
 -30 -25 -20
 Thr Ile Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Leu Leu Pro Val
 -15 -10 -5
 Glu Ala Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe
 1 5 10
 Asp Asp Leu Pro Ala Xaa Phe Gly Tyr Arg Leu Pro Ala Glu Gly Leu
 15 20 25 30
 Lys Gly Phe Leu Ile Asn Ser Lys Pro Glu Asn Ala Cys Glu Pro Ile
 35 40 45
 Val Pro Pro Pro Val Lys Asp Asn Ser Ser Gly Thr Phe Ile Val Leu
 50 55 60
 Ile Xaa Xaa Leu Asp Cys Asn Phe Asp Ile Lys Val Leu Asn Ala Gln
 65 70 75
 Arg Ala Gly Tyr Lys Ala Ala Ile Val His Asn Val Asp Ser Asp Asp
 80 85 90
 Leu Ile Ser Met Gly Ser Asn Asp Ile Glu Val Leu Lys Lys Ile Asp
 95 100 105 110
 Ile Pro Ser Val Phe Ile Gly Glu Ser Ser Ala Ser Ser Leu Lys Asp
 115 120 125
 Glu Phe Thr Xaa Glu Lys Gly Gly His Leu Ile Leu Val Pro Glu Phe
 130 135 140
 Ser Leu Pro Leu Glu Tyr Tyr Leu Ile Pro Phe Leu Ile Xaa Val Gly
 145 150 155

Ile	Cys	Leu	Ile	Leu	Ile	Val	Ile	Phe	Met	Ile	Thr	Lys	Leu	Ser	Arg
160						165					170				
Asp	Arg	His	Arg	Ala	Arg	Arg	Asn	Arg	Leu	Arg	Lys	Asp	Gln	Leu	Lys
175					180					185					190
Lys	Leu	Pro	Val	His	Lys	Phe	Lys	Lys	Gly	Asp	Glu	Tyr	Asp	Val	Cys
				195					200					205	
Ala	Ile	Cys	Leu	Asp	Glu	Tyr	Glu	Asp	Gly	Asp	Lys	Leu	Arg	Ile	Leu
			210					215					220		
Pro	Cys	Ser	His	Ala	Tyr	His	Cys	Lys	Cys	Val	Asp	Pro	Trp	Leu	Thr
		225					230					235			
Lys	Thr	Lys	Lys	Thr	Cys	Pro	Val	Cys	Arg	Gln	Lys	Val	Val	Pro	Ser
	240					245					250				
Gln	Gly	Asp	Ser	Asp	Ser	Asp	Thr	Asp	Ser	Ser	Gln	Glu	Glu	Asn	Glu
255					260					265					270
Val	Thr	Glu	His	Thr	Pro	Leu	Leu	Arg	Pro	Leu	Xaa	Phe	Cys	Gln	Cys
				275					280					285	
Pro	Xaa	Xaa	Phe	Gly	Ala	Leu	Xaa	Gly	Xaa	Pro	Ala	His	Xaa	Gln	Xaa
			290					295					300		
His	Asp	Arg	Ile	Ile	Gln	Thr	Xaa	Glu	Glu	Asp	Asp	Asn	Glu	Asp	Thr
	305					310						315			
Asp	Ser	Ser	Asp	Ala	Glu	Glu									
	320					325									

<210> 107

<211> 291

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42..-1

<400> 107

Met	Asp	Ser	Arg	Val	Ser	Ser	Pro	Glu	Lys	Gln	Asp	Lys	Glu	Asn	Phe
	-40						-35					-30			
Val	Gly	Val	Asn	Asn	Lys	Arg	Leu	Gly	Val	Cys	Gly	Trp	Ile	Leu	Phe
	-25					-20					-15				
Ser	Leu	Ser	Phe	Leu	Leu	Val	Ile	Ile	Thr	Phe	Pro	Ile	Ser	Ile	Trp
-10					-5				1				5		
Met	Cys	Leu	Lys	Ile	Ile	Lys	Glu	Tyr	Glu	Arg	Ala	Val	Val	Phe	Arg
		10					15					20			
Leu	Gly	Arg	Ile	Gln	Ala	Asp	Lys	Ala	Lys	Gly	Pro	Gly	Leu	Ile	Leu
	25					30					35				
Val	Leu	Pro	Cys	Ile	Asp	Val	Phe	Val	Lys	Val	Asp	Leu	Arg	Thr	Val
	40				45						50				
Thr	Cys	Asn	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Arg	Asp	Ser	Val	Thr
55					60					65					70
Thr	Gln	Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Ile	Tyr	Ser	Ala	Val	Ser
			75					80						85	
Ala	Val	Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe	Leu	Leu	Ala
		90						95					100		
Gln	Thr	Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Gln	Thr	Leu	Ser	Gln	Ile
	105						110					115			
Leu	Ala	Gly	Arg	Glu	Glu	Ile	Ala	His	Ser	Ile	Gln	Thr	Leu	Leu	Asp
	120					125					130				
Asp	Ala	Thr	Glu	Leu	Trp	Gly	Ile	Arg	Val	Ala	Arg	Val	Glu	Ile	Lys
135					140					145					150

Asp Val Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala
 155 160 165
 Glu Ala Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu
 170 175 180
 Met Ser Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu
 185 190 195
 Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val
 200 205 210
 Ala Thr Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile
 215 220 225 230
 Leu Glu Gly Ile Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro
 235 240 245
 Asn Lys Ala

<210> 108
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 108
 Met Ser Thr Trp Leu Leu Leu Ile Ala Leu Lys Thr Leu Ile Thr Trp
 -25 -20 -15
 Val Ser Leu Phe Ile Asp Cys Val Met Thr Arg Lys Leu Thr Asn Cys
 -10 -5 1 5
 Asn Ala Arg Glu Thr Ile Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn
 10 15 20
 Cys Phe Ala Ile Arg His Phe Glu Asn Lys Phe Ala Val Glu Thr Leu
 25 30 35
 Ile Cys Ser
 40

<210> 109
 <211> 127
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -63..-1

<400> 109
 Met Ser Ala Ala Gly Ala Arg Gly Leu Arg Ala Thr Tyr His Arg Leu
 -60 -55 -50
 Leu Asp Lys Val Glu Leu Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr
 -45 -40 -35
 Asn His Pro Ala Gly Pro Arg Thr Val Phe Phe Trp Ala Pro Ile Met
 -30 -25 -20
 Lys Trp Gly Leu Val Cys Ala Gly Leu Ala Asp Met Ala Arg Pro Ala
 -15 -10 -5 1
 Glu Lys Leu Ser Thr Ala Gln Ser Ala Val Leu Met Ala Thr Gly Phe
 5 10 15
 Ile Trp Ser Arg Tyr Ser Leu Val Ile Ile Pro Lys Asn Trp Ser Leu

	20					25				30					
Phe	Ala	Val	Asn	Phe	Phe	Val	Gly	Ala	Ala	Gly	Ala	Ser	Gln	Leu	Phe
	35					40				45					
Arg	Ile	Trp	Arg	Tyr	Asn	Gln	Glu	Leu	Lys	Ala	Lys	Ala	His	Lys	
50					55					60					

<210> 110
 <211> 97
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 110
 Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
 -20 -15 -10 -5
 Thr Ala Trp Ala Arg Arg Ser Arg Asp Leu His Cys Gly Ala Cys Arg
 1 5 10
 Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
 15 20 25
 Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln
 30 35 40
 Ser Val Val Glu Val Thr Val Thr Xaa Ser Pro Lys Thr Lys Val Ala
 45 50 55 60
 His Ser Gly Phe Trp Met Lys Ile Arg Leu Leu Lys Lys Gly Pro Trp
 65 70 75
 Ser

<210> 111
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 111
 Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
 -20 -15 -10 -5
 Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
 1 5 10
 Ala Leu Val Asp Glu Thr Arg Met Gly Asn Cys Pro Gly Gly Pro Gln
 15 20 25
 Glu Asp His Ser Asp Gly Ile Phe Pro Asp Gln Ser Arg Trp Gln Pro
 30 35 40
 Val Ser Gly Gly Gly Ala Leu Cys Pro Leu Arg Gly Pro Pro His Arg
 45 50 55 60
 Ala Ala Gly Gly Asp Met
 65

<210> 112
 <211> 71

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 112

Met	Pro	Ala	Gly	Val	Pro	Met	Ser	Thr	Tyr	Leu	Lys	Met	Phe	Ala	Ala
-25					-20					-15					-10
Ser	Leu	Leu	Ala	Met	Cys	Ala	Gly	Ala	Glu	Val	Val	His	Arg	Tyr	Tyr
				-5					1				5		
Arg	Pro	Asp	Leu	Thr	Ile	Pro	Glu	Ile	Pro	Pro	Lys	Arg	Gly	Glu	Leu
	10						15					20			
Lys	Thr	Glu	Leu	Leu	Gly	Leu	Lys	Glu	Arg	Lys	His	Lys	Pro	Gln	Val
	25					30					35				
Ser	Gln	Gln	Glu	Glu	Leu	Lys									
40					45										

<210> 113
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 113

Met	Asp	Gly	His	Trp	Ser	Ala	Ala	Phe	Ser	Ala	Leu	Thr	Val	Thr	Ala
	-40					-35						-30			
Met	Ser	Ser	Trp	Ala	Arg	Arg	Arg	Ser	Ser	Ser	Ser	Arg	Arg	Ile	Pro
	-25				-20						-15				
Ser	Leu	Pro	Gly	Ser	Pro	Val	Cys	Trp	Ala	Trp	Pro	Trp	Tyr	Pro	Asp
-10					-5				1				5		
Thr	Thr	Ser	Phe	Pro	Leu	Arg	Cys	Arg	Gly	Arg	Val				
			10					15							

<210> 114
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -83..-1

<400> 114

Met	Leu	Pro	Val	Gln	Ser	Phe	Thr	Leu	Val	Ala	Gln	Ala	Gly	Val	Gln
			-80					-75					-70		
Trp	Arg	His	Leu	Ser	Ser	Leu	Gln	Leu	Leu	Pro	Pro	Glu	Phe	Lys	Gly
		-65				-60						-55			
Phe	Ser	Cys	Leu	Ser	Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Arg	Arg	Pro	Pro
-50					-45					-40					
Pro	Cys	Pro	Ala	Gly	Phe	Val	Phe	Leu	Val	Glu	Thr	Gly	Leu	His	
-35					-30				-25					-20	

His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Cys Ser Pro Pro
-15 -10 -5
Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val Ser His Val Pro
1 5 10
Gly Lys Lys Lys Leu Leu Lys Val Glu Lys Lys Asn Leu Arg Xaa Leu
15 20 25
Leu Thr Xaa Ile Lys Thr
30 35

<210> 115
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 115
Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
-20 -15 -10
Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
-5 1 5 10
Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Xaa Phe Gly Lys Ala
15 20 25
Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Val Cys Gly Arg Gly
30 35 40
Xaa Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu Phe
45 50

<210> 116
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -52..-1

<400> 116
Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys Asp
-50 -45 -40
Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala
-35 -30 -25
Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu Leu
-20 -15 -10 -5
Val Ser Leu Gly Gln Ser Ile Trp Leu His Ile Thr Glu Asn Gln Ile
1 5 10
Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu Lys
15 20 25
Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
30 35 40

<210> 117
<211> 82
<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -22..-1

<400> 117

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Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
   -20               -15               -10
Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
   -5               1               5               10
Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala
               15               20               25
Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Tyr Gly Pro Ile Phe
               30               35               40
Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe Val Thr Glu Glu Gly
   45               50               55
Arg Asn
   60
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<210> 118

<211> 89

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 118

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Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
   -15               -10               -5
Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
   1               5               10               15
Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
               20               25               30
Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile
               35               40               45
Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala
   50               55               60
Glu Ala Gly Ala Ser Leu Tyr Ser Pro
   65               70
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<210> 119

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19..-1

<400> 119

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Met Thr Met Ala Glu Cys Pro Thr Leu Cys Val Ser Ser Ser Pro Ala
               -15               -10               -5
Leu Trp Ala Ala Ser Glu Thr Thr Asp Asp Val Cys Arg Glu
```


1

5

10

<210> 120
 <211> 115
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -103..-1

<400> 120
 Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile
 -100 -95 -90
 Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile
 -85 -80 -75
 Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp
 -70 -65 -60
 Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Asn Pro
 -55 -50 -45 -40
 Leu Pro Pro Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr Asp
 -35 -30 -25
 Ala Phe Phe Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu Gly
 -20 -15 -10
 Leu Thr Ala Pro Ser Gly Ser Lys Glu Ala Gly Arg Cys Lys Gln Ser
 -5 1 5
 Ser Lys Pro
 10

<210> 121
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -76..-1

<400> 121
 Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr Leu Leu Leu Lys Trp
 -75 -70 -65
 Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp Leu Val Ser Tyr Pro
 -60 -55 -50 -45
 Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn Leu Asp Phe Pro Lys
 -40 -35 -30
 Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr Arg Trp Phe Asn Leu
 -25 -20 -15
 Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala Ser Ser Ser Ala Asn
 -10 -5 1
 Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro Leu Phe Glu
 5 10 15 20
 Glu Leu Arg Gln Val Val Glu Val Ser
 25

<210> 122

<211> 93
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 122
 Met Lys Pro Val Leu Pro Leu Gln Phe Leu Val Val Phe Cys Leu Ala
 -20 -15 -10
 Leu Gln Leu Val Pro Gly Ser Pro Lys Gln Arg Val Leu Lys Tyr Ile
 -5 1 5 10
 Leu Glu Pro Pro Pro Cys Ile Ser Ala Pro Glu Asn Cys Thr His Leu
 15 20 25
 Cys Thr Met Gln Glu Asp Cys Glu Lys Gly Phe Gln Cys Cys Ser Ser
 30 35 40
 Phe Cys Gly Ile Val Cys Ser Ser Glu Thr Phe Gln Lys Arg Asn Arg
 45 50 55
 Ile Lys His Lys Gly Ser Glu Val Ile Met Pro Ala Asn
 60 65 70

<210> 123
 <211> 109
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

<400> 123
 Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
 -40 -35 -30
 Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
 -25 -20 -15
 Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Ala Ile Ile
 -10 -5 1 5
 Leu Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser
 10 15 20
 Ala Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys
 25 30 35
 Val Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met
 40 45 50
 Glu Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Gly Val
 55 60 65

<210> 124
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 124

Met Arg Leu Val Pro Leu Gly Gln Ser Phe Pro Leu Ser Glu Pro Arg
-15 -10 -5 1
Cys Leu Gln Pro Val Lys Trp Asp His Asn His Cys Leu Thr Ser Leu
5 10 15
Thr Val Val Val Arg Thr Glu Cys Val Glu Val Phe His Lys Leu Trp
20 25 30
Met Leu Val
35

<210> 125

<211> 56

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27..-1

<400> 125

Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu
-25 -20 -15
Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg
-10 -5 1 5
Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val Arg Ala
10 15 20
Trp Cys Ile Gln Pro Trp Ala Lys
25

<210> 126

<211> 162

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21..-1

<400> 126

Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
-20 -15 -10
Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
-5 1 5 10
Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala
15 20 25
Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Ser
30 35 40
Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly
45 50 55
Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His
60 65 70 75
Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp
80 85 90
Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val
95 100 105
Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro

110 115 120
 His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val
 125 130 135
 Arg Arg
 140

<210> 127
 <211> 126
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -68..-1

<400> 127
 Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
 -65 -60 -55
 Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
 -50 -45 -40
 His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
 -35 -30 -25
 Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
 -20 -15 -10 -5
 Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
 1 5 10
 Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
 15 20 25
 Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
 30 35 40
 Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Thr Ala
 45 50 55

<210> 128
 <211> 140
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40..-1

<400> 128
 Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
 -40 -35 -30 -25
 Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
 -20 -15 -10
 Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu Glu His
 -5 1 5
 Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
 10 15 20
 Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
 25 30 35 40
 Gly Val Ser Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu
 45 50 55
 Gly Glu Asp Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

				-15					-10					-5			
Asp	Leu	Gly	Arg	Ser	Val	Ile	Ala	Gly	Leu	Trp	Pro	His	Thr	Gly	Val		
			1				5					10					
Leu	Ile	His	Leu	Glu	Thr	Ser	Gln	Ser	Phe	Leu	Gln	Gly	Gln	Leu	Thr		
	15					20					25						
Lys	Ser	Ile	Phe	Pro	Leu	Cys	Cys	Thr	Ser	Leu	Phe	Cys	Val	Cys	Val		
	30				35					40					45		
Val	Thr	Val	Gly	Gly	Arg	Val	Gly	Ser	Thr	Phe	Val	Ala					
			50					55									

<210> 132
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47..-1

Met	Arg	Leu	Pro	Pro	Ala	Leu	Pro	Ser	Gly	Tyr	Thr	Asp	Ser	Thr	Ala		
		-45					-40					-35					
Leu	Glu	Gly	Leu	Val	Tyr	Tyr	Leu	Asn	Gln	Lys	Leu	Leu	Phe	Ser	Ser		
	-30					-25					-20						
Pro	Ala	Ser	Ala	Leu	Leu	Phe	Phe	Ala	Arg	Pro	Cys	Val	Phe	Cys	Phe		
	-15				-10				-5						1		
Lys	Ala	Ser	Lys	Met	Gly	Pro	Gln	Phe	Glu	Asn	Tyr	Pro	Thr	Phe	Pro		
		5					10						15				
Thr	Tyr	Ser	Pro	Leu	Pro	Ile	Ile	Pro	Phe	Gln	Leu	His	Gly	Arg	Phe		
		20				25						30					

<210> 133
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

Met	Asp	Ser	Arg	Val	Ser	Ser	Pro	Glu	Lys	Gln	Asp	Lys	Glu	Asn	Phe		
	-40					-35					-30						
Val	Gly	Val	Asn	Asn	Lys	Arg	Leu	Gly	Val	Cys	Gly	Trp	Ile	Leu	Phe		
	-25				-20					-15							
Ser	Leu	Ser	Phe	Leu	Leu	Val	Ile	Ile	Thr	Phe	Pro	Ile	Ser	Ile	Trp		
	-10				-5				1				5				
Met	Cys	Leu	Lys	Ile													
		10															

<210> 134
 <211> 1053
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 131..169
 <223> Von Heijne matrix
 score 4.19999980926514
 seq MLAVSLTVPLLGA/MM

<221> polyA_site
 <222> 1042..1053

<400> 134

gagcagagtcg	gacgggctgc	gacagcgccg	gcccctgcgg	ccgcaggtcg	tcacagacga	60
tgatggccag	gccccggagg	ctaaggacgg	cagctccttt	agcggcagag	ttttccgagt	120
gaccttcttg	atg ctg gct gtt tct ctc acc gtt ccc ctg ctt gga gcc	169				
	Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala					
	-10		-5			
atg atg ctg ctg gaa tct cct ata gat cca cag cct ctc agc ttc aaa	217					
Met Met Leu Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys						
1 5 10 15						
gaa ccc ccg ctc ttg ctt ggt gtt ctg cat cca aat acg aag ctg cga	265					
Glu Pro Pro Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg						
20 25 30						
cag gca gaa agg ctg ttt gaa aat caa ctt gtt gga ccg gag tcc ata	313					
Gln Ala Glu Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile						
35 40 45						
gca cat att ggg gat gtg atg ttt act ggg aca gca gat ggc cgg gtc	361					
Ala His Ile Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val						
50 55 60						
gta aaa ctt gaa aat ggt gaa ata gag acc att gcc cgg ttt ggt tcg	409					
Val Lys Leu Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser						
65 70 75 80						
ggc cct tgc aaa acc cga ggt gat gag cct gtg tgt ggg aga ccc ctg	457					
Gly Pro Cys Lys Thr Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu						
85 90 95						
ggt atc cgt gca ggg ccc aat ggg act ctc ttt gtg gcc gat gca tac	505					
Gly Ile Arg Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Tyr						
100 105 110						
aag gga cta ttt gaa gta aat ccc tgg aaa cgt gaa gtg aaa ctg ctg	553					
Lys Gly Leu Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu						
115 120 125						
ctg tcc tcc gag aca ccc att gag ggg aag aac atg tcc ttt gtg aat	601					
Leu Ser Ser Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn						
130 135 140						
gat ctt aca gtc act cag gat ggg agg aag att tat ttc acc gat tct	649					
Asp Leu Thr Val Thr Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser						
145 150 155 160						
agc agc aaa tgg caa aga cga gac tac ctg ctt ctg gtg atg gag ggc	697					
Ser Ser Lys Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met Glu Gly						
165 170 175						
aca gat gac ggg cgc ctg ctg gag tat gat act gtg acc agg gaa gta	745					
Thr Asp Asp Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val						
180 185 190						
aaa gtt tta ttg gac cag ctg cgg ttc ccg aat gga gtc cag ctg tct	793					
Lys Val Leu Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser						
195 200 205						
cct gca gaa gac ttt gtc ctg gtg gca gaa aca acc atg gcc agg ata	841					
Pro Ala Glu Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile						
210 215 220						

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cga aga gtc tac gtt tct ggc ctg atg aag ggc ggg gct gat ctg ttt      889
Arg Arg Val Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe
225                230                235                240
gtg gag aac atg cct gga ttt cca gac aac atc cgg ccc agc agc tct      937
Val Glu Asn Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser
                245                250                255
ggg ggg tac tgg gtg ggc atg tcg acc atc cgc cct aac cct ggg ttt      985
Gly Gly Tyr Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe
                260                265                270
tcc atg ctg gat ttc tta tct gag aga ccc tgg att aaa agg atg att      1033
Ser Met Leu Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile
                275                280                285
ttt aag gta aaaaaaaaaa a
Phe Lys Val
290

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<210> 135
<211> 675
<212> DNA
<213> Homo sapiens

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<220>
<221> polyA_signal
<222> 638..643
<221> polyA_site
<222> 662..675
<400> 135
accgaacagg aacagcacaa cctgggaccc agacatgcag tacctctacg caaagtaaaa      60
gtagcagtggt ttcagcacac tttggtatgt tgactgtta atg atg tac gtt tct      114
                               Met Met Tyr Val Ser
                               1             5
ata gaa atg tca ggt cca acc att tcc cat ttg ttc gac tat gtg gtc      162
Ile Glu Met Ser Gly Pro Thr Ile Ser His Leu Phe Asp Tyr Val Val
                10                15                20
tgt tac att tat ggc tta aag tcc ttt tct ctt aaa cag tta aaa aaa      210
Cys Tyr Ile Tyr Gly Leu Lys Ser Phe Ser Leu Lys Gln Leu Lys Lys
                25                30                35
aaa tct tgg tct aag tat tta ttt gaa tcc tgt tgc tat agg agt ttg      258
Lys Ser Trp Ser Lys Tyr Leu Phe Glu Ser Cys Cys Tyr Arg Ser Leu
                40                45                50
tat gtg tgt gtc ttc att taaacatacc tgcatacaaa gatggtttat      306
Tyr Val Cys Val Phe Ile
55
ttctattttaa tatgtgacat ttgtttcctg gatatagtcg gtgaaccaca agatttatca      366
tatttttcaa taatagaga agaaaatggg ccgtaaattg ttaaccattt tatgttcaga      426
tatttctcta gtttttacct agtttgcttt aacatagaga ccagcaagtg aatatatatg      486
cataacctta tatgtgaca caataattca gaataatttg ttaaagataa actaattttt      546
cagagaagaa catTTaaagg gttaatatTT ttgaaacggt ttcagataat atctatttga      606
ttattgtggc ttctatttga aatgtgtcta aaataaatgc tgtttattta aaatgaaaaa      666
aaaaaaaaa
675

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<210> 136
<211> 1112
<212> DNA

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<213> Homo sapiens

<220>

<221> sig_peptide

<222> 111..194

<223> Von Heijne matrix

score 4.80000019073486

seq GVLLEPFVHQVGG/HS

<221> polyA_signal

<222> 1080..1085

<221> polyA_site

<222> 1101..1112

<400> 136

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ccgagagaga ctacacggta ctgggacaca cggacaaaca acagacagaa gacgtactgg      60
ccgctggact ccgtgcctc ccccatctcc ccgccatctg cgcccggagg atg agc      116
                                     Met Ser
cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt      164
Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu
  -25                -20                -15
ctg gag ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc      212
Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg
  -10                -5                1                5
ttc aat gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag      260
Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln
                10                15                20
ttc tac gag acc ctc cct gct gag atg cgc aaa ttc tct ccc cag tac      308
Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Ser Pro Gln Tyr
                25                30                35
aaa gga caa agc caa agg ccc ctt gtt agc tgg cca tcc ctg ccc cat      356
Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp Pro Ser Leu Pro His
                40                45                50
ttt ttc ccc tgg tcc ttt ccc ctg tgg cca cag gga agt gtg gcc      401
Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln Gly Ser Val Ala
                55                60                65
tgaatacccc accccggctc ctctgcaccc agagctgggg gccacctcag aagtgtcatc      461
tctctctgag cagcattcc cctgcagcag tcgaggactg agcagattga gtgatgctgg      521
ggcagagagg cctgagagga aaggtgttca gccagtcgtt tgtaaggcgc tcgtcggcac      581
ctgctgaaac gccccacct gacagcccca tcctcaaaga ctgtcttaat tactcatggc      641
aggttctaga gacttaaggg gaaaagctgc tttcaaggcc accacatgtc tgtgctcccc      701
aaccagctct atctgccttg tgttcatttt gttattttgt gacgtgagac agcaaagacc      761
aataaaaaca tattttataa gaacaaaagg cctgggtgcc taccogtggt ggggcactgt      821
gggaagcctt tgctagggtg tcttggtgctg tgtggtttgt tttgtttgcc cctttatttt      881
gctttgctta cccagtcttc ccttactott ggatgcttct taaccctcag gcaaacctgt      941
gttccccctg tattcaggct ctgctttaaa gcaagccatg aggctgttgg agtttctgtt     1001
tagggcatta aaaattcccg caaactataa agagcaatgt tttcagtcct ttaggattag     1061
aagaattaca taaaaattaa taaacatttt caatgatgga aaaaaaaaaa a      1112
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<210> 137

<211> 547

<212> DNA

<213> Homo sapiens

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<221> sig_peptide

<222> 359..454
 <223> Von Heijne matrix
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 seq FSFMLLGMGCLP/GF

<221> polyA_site
 <222> 536..547

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 cagctagcct ctcatccctt ttctactgag aggaagtggg atgcactccg acaaggataa 120
 ggttttattg tgagctggcc ttggaattaa accaccacca acacactttt ggattatcag 180
 aaggtggaag gagtgcaaaa atgtcattcc catgcttgct tgccaggcaa cctggtgtcc 240
 attctttatg acgcctttcc tgaatcacag gtgcattggg gtgcttcctc ctccccagga 300
 ctcccaccca actttgtgaa cacaaccac ttagaggagt tatctcagca cattatga 358
 atg ttg ggg acc acg ggc ctc ggg aca cag ggt cct tcc cag cag gct 406
 Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala
 -30 -25 -20
 ctg ggc ttt ttc tcc ttt atg tta ctt gga atg ggc ggg tgc ctg cct 454
 Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro
 -15 -10 -5
 gga ttc ctg cta cag cct ccc aat cga tct cct act ttg cct gca tcc 502
 Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser
 1 5 10 15
 acc ttt gcc cat taaagtcaat tctccacca taaaaaaaaa aaa 547
 Thr Phe Ala His
 20

<210> 138
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 26..316
 <223> Von Heijne matrix
 score 4
 seq RLPLVVVSFIASSS/AN

<221> polyA_signal
 <222> 1164..1169

<221> polyA_site
 <222> 1187..1198

<400> 138
 atcctgcgaa agaaggggggt tcatac atg gcg gat gac cta aag cga ttc ttg 52
 Met Ala Asp Asp Leu Lys Arg Phe Leu
 -95 -90
 tat aaa aag tta cca agt gtt gaa ggg ctc cat gcc att gtt gtg tca 100
 Tyr Lys Lys Leu Pro Ser Val Glu Gly Leu His Ala Ile Val Val Ser
 -85 -80 -75
 gat aga gat gga gta cct gtt gtt aaa gtg gca aat gac aat gct cca 148
 Asp Arg Asp Gly Val Pro Val Val Lys Val Ala Asn Asp Asn Ala Pro
 -70 -65 -60
 gag cat gct ttg cga cct ggt ttc tta tcc act ttt gcc ctt gca aca 196

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Glu His Ala Leu Arg Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr
-55 -50 -45
gac caa gga agc aaa ctt gga ctt tcc aaa aat aaa agt atc atc tgt 244
Asp Gln Gly Ser Lys Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys
-40 -35 -30 -25
tac tat aac acc tac cag gtg gtt caa ttt aat cgt tta cct ttg gtg 292
Tyr Tyr Asn Thr Tyr Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val
-20 -15 -10
gtg agt ttc ata gcc agc agc agt gcc aat aca gga cta att gtc agc 340
Val Ser Phe Ile Ala Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser
-5 1 5
cta gaa aag gag ctt gct cca ttg ttt gaa gaa ctg aga caa gtt gtg 388
Leu Glu Lys Glu Leu Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val
10 15 20
gaa gtt tct taatctgaca gtggtttcag tgtgtacctt atcttcatta 437
Glu Val Ser
25
taacaacaca atatcaatcc agcaatcttt agactacaat aatgctttta tccatgtgct 497
caagaaaggg cccctttttc caacttatac taaagagcta gcatatagat gtaatttata 557
gatagatcag ttgctatatt ttctgggtga gggctctttct tatttagtga gatctaggga 617
taccacagaa atgggttcagt ctatcacagc tcccatggag ttagtctggg caccagatat 677
ggatgagaga ttctatttcag tggattagaa tcaaactggt acattgatcc acttgagccg 737
ttaagtgtcg ccaattgtac aatatgccca ggcttgacaga ataaagccaa ctttttattg 797
tgaataataa taaggacata tttttcttca gattatgttt tatttctttg cattgagtga 857
ggtacataaaa atggcttggt aaaagtaata aaatcagtag aatcactaac tttcctttgt 917
acatattatt ttgcagtata gatgaatatt actaatcagt ttgattattc tcagagggtg 977
ctgctcttta atgaaaatga aaattatagc taatgttttt tcctcaaact ctgctttctg 1037
taaccaatca gtgttttaat gtttgtgtgt tcttcataaaa atttaaatac aattcgttat 1097
tctgtttcca atgttagtat gtatgtaaac atgatagtac agccattttt ttcatatgtg 1157
agtaaaaata aaatagtatt tttaaaagta aaaaaaaaaa a 1198

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<211> 1400
<212> DNA
<213> Homo sapiens

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<222> 36..107
<223> Von Heijne matrix
score 5.69999980926514
seq ILGLLGLLGLTIVA/ML

<221> polyA_signal
<222> 1302..1307

<221> polyA_site
<222> 1389..1400

<400> 139
cagtccctga agacgcttct actgagaggt ctgcc atg gcc tct ctt ggc ctc 53
Met Ala Ser Leu Gly Leu
-20
caa ctt gtg ggc tac atc cta ggc ctt ctg ggg ctt ttg ggc aca ctg 101
Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu Gly Leu Leu Gly Thr Leu
-15 -10 -5
gtt gcc atg ctg ctc ccc agc tgg aaa aca agt tct tat gtc ggt gcc 149

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Val	Ala	Met	Leu	Leu	Pro	Ser	Trp	Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala		
	1					5					10						
agc	att	gtg	aca	gca	gtt	ggc	ttc	tcc	aag	ggc	ctc	tgg	atg	gaa	tgt		197
Ser	Ile	Val	Thr	Ala	Val	Gly	Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys		
15					20					25				30			
gcc	aca	cac	agc	aca	ggc	atc	acc	cag	tgt	gac	atc	tat	agc	acc	ctt		245
Ala	Thr	His	Ser	Thr	Gly	Ile	Thr	Gln	Cys	Asp	Ile	Tyr	Ser	Thr	Leu		
				35					40					45			
ctg	ggc	ctg	ccc	gct	gac	atc	cag	gct	gcc	cag	gcc	atg	atg	gtg	aca		293
Leu	Gly	Leu	Pro	Ala	Asp	Ile	Gln	Ala	Ala	Gln	Ala	Met	Met	Val	Thr		
			50					55					60				
tcc	agt	gca	atc	tcc	tcc	ctg	gcc	tgc	att	atc	tct	gtg	gtg	ggc	atg		341
Ser	Ser	Ala	Ile	Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	Met		
	65						70					75					
aga	tgc	aca	gtc	ttc	tgc	cag	gaa	tcc	cga	gcc	aaa	gac	aga	gtg	gcg		389
Arg	Cys	Thr	Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala		
	80					85					90						
gta	gca	ggg	gga	gtc	ttt	ttc	atc	ctt	gga	ggc	ctc	ctg	gga	ttc	att		437
Val	Ala	Gly	Gly	Val	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile			
95				100					105					110			
cct	gtt	gcc	tgg	aat	ctt	cat	ggg	atc	cta	cgg	gac	ttc	tac	tca	cca		485
Pro	Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro		
				115					120				125				
ctg	gtg	cct	gac	agc	atg	aaa	ttt	gag	att	gga	gag	gct	ctt	tac	ttg		533
Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr	Leu		
			130					135				140					
ggc	att	att	tct	tcc	ctg	ttc	tcc	ctg	ata	gct	gga	atc	atc	ctc	tgc		581
Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile	Leu	Cys		
	145					150					155						
ttt	tcc	tgc	tca	tcc	cag	aga	aat	cgc	tcc	aac	tac	tac	gat	gcc	tac		629
Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr	Asp	Ala	Tyr		
	160					165					170						
caa	gcc	caa	cct	ctt	gcc	aca	agg	agc	tct	cca	agg	cct	ggg	caa	cct		677
Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg	Pro	Gly	Gln	Pro		
	175				180						185			190			
ccc	aaa	gtc	aag	agt	gag	ttc	aat	tcc	tac	agc	ctg	aca	ggg	tat	gtg		725
Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr	Ser	Leu	Thr	Gly	Tyr	Val		
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<211> 538

<212> DNA

<213> Homo sapiens

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<221> polyA_signal
 <222> 505..510

<221> polyA_site
 <222> 526..538

<400> 140

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cgt gct ttt cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg      103
Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu
-25                               -20                               -15                               -10
ttg ctg att gct gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc      151
Leu Leu Ile Ala Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile
                               -5                               1                               5
cga tat gat gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa      199
Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys
                               10                               15                               20
ccg aaa gag aat aaa ata tct tta gag tcg gaa tat gag gga agt atc      247
Pro Lys Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Gly Ser Ile
                               25                               30                               35
tgt tgaagggcta ctatctttcc ttggcccttc tcccttggtg ggactcaatc      300
Cys
40
tccagactat ctccccagag aatcttgtca aggcttggt ttaagctttg ttgggaaaat      360
caaagactcc aagtttgatg actggaagaa tattcgagga cccaggcctt gggaagatcc      420
tgacctcctc caaggaagaa atccagaaag ccttaagact aagacaactt gactctgctg      480
attctttttt cctttttttt tttaaataaa aatactatta actggaaaaa aaaaaaaaa      538

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<210> 141
 <211> 1167
 <212> DNA
 <213> Homo sapiens

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 <222> 169..267
 <223> Von Heijne matrix
 score 7.80000019073486
 seq LTFLEFLHLPPTS/LF

<221> polyA_signal
 <222> 1132..1137

<221> polyA_site
 <222> 1155..1167

<400> 141

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gtaggaacta ctgtcccaga gctgaggcaa ggggatttct caggtcattt ggagaacaag      60
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gaaatttgaa gaccagatca tgggtggtct gcatgtgaat gaacagga atg agc cag      177
                                   Met Ser Gln
aca gcc tgg ctg tca ttg ctt tct tcc tcc cca ttt gga ccc ttc tct      225
Thr Ala Trp Leu Ser Leu Leu Ser Ser Ser Pro Phe Gly Pro Phe Ser
-30          -25          -20          -15
gcc ctt aca ttt ttg ttt ctc cat cta cca cca tcc acc agt cta ttt      273
Ala Leu Thr Phe Leu Phe Leu His Leu Pro Pro Ser Thr Ser Leu Phe
          -10          -5          1
att aac tta gca aga gga caa ata aag ggc cct ctt ggc ttg att ttg      321
Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly Pro Leu Gly Leu Ile Leu
          5          10          15
ctt ctt tct ttc tgt gga gga tat act aag tgc gac ttt gcc cta tcc      369
Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys Cys Asp Phe Ala Leu Ser
          20          25          30
tat ttg gaa atc cct aac aga att gag ttt tct att atg gat cca aaa      417
Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe Ser Ile Met Asp Pro Lys
          35          40          45          50
aga aaa aca aaa tgc taatgaagcc atcagtcaag ggtcacatgc caataaacia      472
Arg Lys Thr Lys Cys
          55
taaattttcc agaagaaatg aaatccaact agacaaataa agtagagctt atgaaatggt      532
tcagtaagga tgagcttggt gttttttggt ttgttttggt ttgttttttt aaagacggag      592
tctcgctctg tcaactcaggc tggagtgcag tggtagatgc ttggctcact gtaacctccg      652
cctcccgggt tcaagccatt ctcctgcctc agtctcctga gtagctggga ttgcaggtgc      712
gtgccaccat gcctggctaa tttttgtgtt tttggtagag acagggtttc accacgttgg      772
tcgggctggt ctcgggctcc tgacctcttg atccgcctgc cttggcctcc caaagtgatg      832
ggattacaga tgtgagccac cgtgcctagc caaggatgag atttttaaag tatgttccag      892
ttctgtgtca tgggtggaag acagagtagg aaggatagtg aaaaggtcat ggggaagcag      952
aggtgattca tggctctgtg aatttgaggt gaatggttcc ttattgtcta ggccacttgt      1012
gaagaatatg agtcagttat tgccagcctt ggaatttact tctctagctt acaatggacc      1072
tttttgaactg ggaacacct tgtctgcatt cactttaaaa tgtcaaaaact aatttttata      1132
ataaatgttt attttcacat cgaaaaaaa aaaaaa      1167

<210> 142
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<212> DNA
<213> Homo sapiens

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<221> sig_peptide
<222> 143..238
<223> Von Heijne matrix
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      seq VPMLLLIVGGSFG/LR

<221> polyA_signal
<222> 697..702

<221> polyA_site
<222> 721..730

<400> 142
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cttggtgaga gcgtgagctg ctgagatttg ggagctctgc ctaggcccgc ttggagttct      120
gagccgatgg aagagttcac tc atg ttt gca ccc gcg gtg acg cgt gct ttt      172
              Met Phe Ala Pro Ala Val Thr Arg Ala Phe
              -30          -25

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cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg att	220
Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile	
-20 -15 -10	
gtt gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc cga tat gat	268
Val Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp	
-5 1 5 10	
gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag	316
Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu	
15 20 25	
aat aaa ata tct tta gag tcg gaa tat gag aaa atc aaa gac tcc aag	364
Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys	
30 35 40	
ttt gat gac tgg aag aat att cga gga ccc agg cct tgg gaa gat cct	412
Phe Asp Asp Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro	
45 50 55	
gac ctc ctc caa gga aga aat cca gaa agc ctt aag act aag aca act	460
Asp Leu Leu Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr	
60 65 70	
tgactctgct gattctcttt tccttttttt ttttaaataa aaatactatt aactggactt	520
cctaatatat acttctatca agtggaaagg aaattccagg cccatggaaa cttggatatg	580
ggtaatttga tgacaaataa tcttcactaa aggtcatgta cagggttttta tacttcccag	640
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aaaaatgtga atactgctcc aaaaaaaaaa	730

<210> 143
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 <223> Von Heijne matrix
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 seq SFLPSALVIWTS/AF
 <221> polyA_signal
 <222> 1141..1146
 <221> polyA_site
 <222> 1161..1174

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tgaagactaa cattttgtga agttgtaaaa cagaaaacct gttagaa atg tgg tgg	116
Met Trp Trp	
-20	
ttt cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca	164
Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr	
-15 -10 -5	
tct gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat	212
Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His	
1 5 10	
ata gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca	260
Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro	
15 20 25 30	
gaa aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgc	308

Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys	
35 40 45	
att gct acc att tat gtt cgt tat aag caa gtt cat gct ctg agt cct	356
Ile Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala Leu Ser Pro	
50 55 60	
gaa gag aac gtt atc atc aaa tta aac aag gct ggc ctt gta ctt gga	404
Glu Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu Val Leu Gly	
65 70 75	
ata ctg agt tgt tta gga ctt tct att gtg gca aac ttc cag aaa aca	452
Ile Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe Gln Lys Thr	
80 85 90	
acc ctt ttt gct gca cat gta agt gga gct gtg ctt acc ttt ggt atg	500
Thr Leu Phe Ala Ala His Val Ser Gly Ala Val Leu Thr Phe Gly Met	
95 100 105 110	
ggc tca tta tat atg ttt gtt cag acc atc ctt tcc tac caa atg cag	548
Gly Ser Leu Tyr Met Phe Val Gln Thr Ile Leu Ser Tyr Gln Met Gln	
115 120 125	
ccc aaa atc cat ggc aaa caa gtc ttc tgg atc aga ctg ttg ttg gtt	596
Pro Lys Ile His Gly Lys Gln Val Phe Trp Ile Arg Leu Leu Val	
130 135 140	
atc tgg tgt gga gta agt gca ctt agc atg ctg act tgc tca tca gtt	644
Ile Trp Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys Ser Ser Val	
145 150 155	
ttg cac agt ggc aat ttt ggg act gat tta gaa cag aaa ctc cat tgg	692
Leu His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys Leu His Trp	
160 165 170	
aac ccc gag gac aaa ggt tat gcg ctt cac atg atc act act gca gca	740
Asn Pro Glu Asp Lys Gly Tyr Ala Leu His Met Ile Thr Thr Ala Ala	
175 180 185 190	
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Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu Thr Tyr Ile	
195 200 205	
cgt gat ttt cag aaa att tcc tta cgg gtg gaa gcc aac tta cat gga	836
Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn Leu His Gly	
210 215 220	
tta acc ctc tat gac act gca cct tgc cct att aac aat gaa cga aca	884
Leu Thr Leu Tyr Asp Thr Ala Pro Cys Pro Ile Asn Asn Glu Arg Thr	
225 230 235	
cgg cta ctt tcc aga gat att aga tgaaaggata aaatatttct gtaatgatta	938
Arg Leu Leu Ser Arg Asp Ile Arg	
240 245	
tgattctcag ggattgggga aagggttcaca gaagttgctt attcttctct gaaattttca	998
accacttaat caaggctgac agtaacactg atgaatgctg ataatcagga aacatgaaag	1058
aagccatttg atagattatt cttaaaggata tcatcaagaa gactattaaa aacacctatg	1118
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<210> 144
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 <212> DNA
 <213> Homo sapiens

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 <221> polyA_signal
 <222> 1133..1138

<221> polyA_site
 <222> 1146..1158


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<400> 144
aarttgagct tggggactgc agctgtgggg agatttcagt gcattgcctc ccctgggtgc      60
tcttcatctt ggatttgaaa gttgagagca gcatgttttg cccactgaaa ctcatcctgs    120
tgrsagtgtg mtggattatt ccttgggcct gaatgacttg aatgtttccc cgcctgagct    180
aacagtccat gtgggtgatt cagctctg atg gga tgt gtt ttc cag agc aca      232
                               Met Gly Cys Val Phe Gln Ser Thr
                               1           5
gaa gac aaa tgt ata ttc aag ata gac tgg act ctg tca cca gga gag      280
Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu
   10           15           20
cac gcc aag gac gaa tat gtg cta tac tat tac tcc aat ctc agt gtg      328
His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val
   25           30           35           40
cct att ggg cgc ttc cag aac cgc gta cac ttg atg ggg gac atc tta      376
Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Ile Leu
           45           50           55
tgc aat gat ggc tct ctc ctg ctc caa gat gtg caa gag gct gac cag      424
Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln
           60           65           70
gga acc tat atc tgt gaa atc cgc ctc aaa ggg gag agc cag gtg ttc      472
Gly Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe
           75           80           85
aag aag gcg gtg gta ctg cat gtg ctt cca gag gag ccc aaa ggt acg      520
Lys Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Gly Thr
           90           95          100
caa atg ctt act taaagagggg ccaaggggca agagctttca tgtgcaagag      572
Gln Met Leu Thr
105
gcaaggaaac tgattatctt gagtaaagtc cagccttttg gctaagtact taccacagag      632
tgaatcttca aagaaatgan tcattaaatt atttcagrtc agaataaaaa takgagttat      692
tttagttaak aataaaatat tgataattat tgtattatta ctttaaacac acttccccct      752
cacaaaagcc ctgtgaagga tgttttgttc acatataatg tccaaatatg ttttgacac      812
atattttatta aatggaataa atagtamttg aaccctggca ccthtgacaa caaagtcyat      872
gttyttttta ctatgcccta atacctttsa tcagttatcc acattgatgc tacatytgta      932
ttttataggt accctatgtt aggtgttttg ggggatagaa aagaaataag cagkycaggc      992
tcagtggctc atgcctgtaa tcctagcatt ttggggaggct gaggcagcag aamtgcctga    1052
gccccagggt tcaagactgc agtgagctat gawggcacca ctgcattyta gcctgggwgga    1112
cagagcaaga ctytgtttaa aataaaaaaaaa gagaaaaaaaa aaaaaa                1158

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<210> 145
<211> 754
<212> DNA
<213> Homo sapiens

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<220>
<221> sig_peptide
<222> 5..142
<223> Von Heijne matrix
      score 6.59999990463257
      seq VCCYLFWLIAILA/QL

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<221> polyA_signal
<222> 716..721

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<221> polyA_site
<222> 742..754

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<400> 145
tgtg atg agc gtg ttc tgg ggc ttc gtc ggc ttc ttg gtg cct tgg ttc      49
    Met Ser Val Phe Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe
        -45                -40                -35
atc ccc aag ggt cct aac cgg gga gtt atc att acc atg ttg gtg acc      97
Ile Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr
    -30                -25                -20
tgt tca gtt tgc tgc tat ctc ttt tgg ctg att gca att ctg gcc caa      145
Cys Ser Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln
    -15                -10                -5                1
ctc aac cct ctc ttt gga ccg caa ttg aaa aat gaa acc atc tgg tat      193
Leu Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr
        5                10                15
ctg aag tat cat tgg cct tgaggaagaa gacatgctct acagtgtcga      241
Leu Lys Tyr His Trp Pro
    20
gtcttttgagg tcacgagaag agaatgcctt ctagatgcaa aatcacctct aaaccagacc      301
acttttcttg acttgccctgt tttggccatt agctgcctta aacgttaaca gcacatttga      361
atgccttatt ctacaatgca gcgtgttttc ctttgccttt tttgcacttt ggtgaattac      421
gtgcctccat aacctgaact gtgccgactc cacaaaaacga ttatgtactc ttctgagata      481
gaagatgctg ttcttctgag agatacgta ctctctcctt ggaatctgtg gatttgaaga      541
tggctcctgc cttctcacgt gggaatcagt gaagtgttta gaaactgctg caagacaaac      601
aagactccag tggggtggtc agtaggagag cacgttcaga gggaagagcc atctcaacag      661
aatcgacca aactatactt tcaggatgaa tttcttcttt ctgccatctt ttggaataaa      721
tatttttctc ctttctatgt aaaaaaaaaa aaa      754

<210> 146
<211> 1073
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 98..181
<223> Von Heijne matrix
    score 3.59999990463257
    seq PLSDSWALLPASA/GV

<221> polyA_signal
<222> 1035..1040

<221> polyA_site
<222> 1060..1073

<400> 146
ccgattacag ctaggtagtg gagcgccgct gcttacctgg gtgcaggaga cagccggagt      60
cgctggggga gctccgcgcc gccggacgcc cgtgacc atg tgg agg ctg ctg gct      115
                        Met Trp Arg Leu Leu Ala
                                -25
cgc gct agt gcg ccg ctc ctg cgg gtg ccc ttg tca gat tcc tgg gca      163
Arg Ala Ser Ala Pro Leu Leu Arg Val Pro Leu Ser Asp Ser Trp Ala
    -20                -15                -10
ctc ctc ccc gcc agt gct ggc gta aag aca ctg ctc cca gta cca agt      211
Leu Leu Pro Ala Ser Ala Gly Val Lys Thr Leu Leu Pro Val Pro Ser
    -5                1                5                10
ttt gaa gat gtt tcc att cct gaa aaa ccc aag ctt aga ttt att gaa      259

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Phe	Glu	Asp	Val	Ser	Ile	Pro	Glu	Lys	Pro	Lys	Leu	Arg	Phe	Ile	Glu		
				15					20					25			
agg	gca	cca	ctt	gtg	cca	aaa	gta	aga	aga	gaa	cct	aaa	aat	tta	agt	307	
Arg	Ala	Pro	Leu	Val	Pro	Lys	Val	Arg	Arg	Glu	Pro	Lys	Asn	Leu	Ser		
			30					35					40				
gac	ata	cgg	gga	cct	tcc	act	gaa	gct	acg	gag	ttt	aca	gaa	ggc	aat	355	
Asp	Ile	Arg	Gly	Pro	Ser	Thr	Glu	Ala	Thr	Glu	Phe	Thr	Glu	Gly	Asn		
		45					50					55					
ttt	gca	atc	ttg	gca	ttg	ggg	ggg	ggc	tac	ctg	cat	tgg	ggc	cac	ttt	403	
Phe	Ala	Ile	Leu	Ala	Leu	Gly	Gly	Gly	Tyr	Leu	His	Trp	Gly	His	Phe		
	60					65				70							
gaa	atg	atg	cgc	ctg	aca	atc	aac	cgc	tct	atg	gac	ccc	aag	aac	atg	451	
Glu	Met	Met	Arg	Leu	Thr	Ile	Asn	Arg	Ser	Met	Asp	Pro	Lys	Asn	Met		
75					80					85				90			
ttt	gcc	ata	tgg	cga	gta	cca	gcc	cct	ttc	aag	ccc	atc	act	cgc	aaa	499	
Phe	Ala	Ile	Trp	Arg	Val	Pro	Ala	Pro	Phe	Lys	Pro	Ile	Thr	Arg	Lys		
			95					100						105			
agt	gtt	ggg	cat	cgc	atg	ggg	gga	ggc	aaa	ggg	gct	att	gac	cac	tac	547	
Ser	Val	Gly	His	Arg	Met	Gly	Gly	Gly	Lys	Gly	Ala	Ile	Asp	His	Tyr		
			110					115					120				
gtg	aca	cct	gtg	aag	gct	ggc	cgc	ctt	gtt	gta	gag	atg	ggg	ggg	cgt	595	
Val	Thr	Pro	Val	Lys	Ala	Gly	Arg	Leu	Val	Val	Glu	Met	Gly	Gly	Arg		
		125				130						135					
tgt	gaa	ttt	gaa	gaa	gtg	caa	ggg	ttc	ctt	gac	cag	ggt	gcc	cac	aag	643	
Cys	Glu	Phe	Glu	Glu	Val	Gln	Gly	Phe	Leu	Asp	Gln	Val	Ala	His	Lys		
	140					145				150							
ttg	ccc	ttc	gca	gca	aag	gct	gtg	agc	cgc	ggg	act	cta	gag	aag	atg	691	
Leu	Pro	Phe	Ala	Ala	Lys	Ala	Val	Ser	Arg	Gly	Thr	Leu	Glu	Lys	Met		
155					160					165				170			
cga	aaa	gat	caa	gag	gaa	aga	gaa	cgt	aac	aac	cag	aac	ccc	tgg	aca	739	
Arg	Lys	Asp	Gln	Glu	Glu	Arg	Glu	Arg	Asn	Asn	Gln	Asn	Pro	Trp	Thr		
			175					180					185				
ttt	gag	cga	ata	gcc	act	gcc	aac	atg	ctg	ggc	ata	cgg	aaa	gta	ctg	787	
Phe	Glu	Arg	Ile	Ala	Thr	Ala	Asn	Met	Leu	Gly	Ile	Arg	Lys	Val	Leu		
		190				195						200					
agc	cca	tat	gac	ttg	acc	cac	aag	ggg	aaa	tac	tgg	ggc	aag	ttc	tac	835	
Ser	Pro	Tyr	Asp	Leu	Thr	His	Lys	Gly	Lys	Tyr	Trp	Gly	Lys	Phe	Tyr		
	205					210				215							
atg	ccc	aaa	cgt	gtg	tagtgagtgt	aggagataac	tgtatatagg	ctactgaaag								890	
Met	Pro	Lys	Arg	Val													
	220																
aaggattctg	catttctatt	cccctcagcc	taccactga	agtctttggg	tagctcttaa											950	
gccataacta	aggagcagca	tttgagtaga	tttctgaaaa	acgatgttat	ttgttgattt											1010	
aaaaagaaaa	ctgtattttt	attaaataaa	atttaaacad	cacttcagga	aaaaaaaaaa											1070	
aaa																1073	

<210> 147
 <211> 413
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 46..189
 <223> Von Heijne matrix
 score 4.09999990463257
 seq VFMLIVSVLALIP/ET

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<221> polyA_signal
<222> 377..382

<221> polyA_site
<222> 402..413

<400> 147
tgagaagagt tgagggaaag tgctgctgct gggctctgcag acgcg atg gat aac gtg      57
                                         Met Asp Asn Val
                                         -45
cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg aaa ggc cac      105
Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val Lys Gly His
          -40                      -35                      -30
gtg aag atg ctg cgg ctg gat att atc aac tca ctg gta aca aca gta      153
Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val
          -25                      -20                      -15
ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa acc aca aca      201
Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
          -10                      -5                      1
ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca gta tgc tgc      249
Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys
5          10          15          20
ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc agc      297
Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser
          25          30          35
ggg cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa gtt ttg      342
Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
          40          45          50
taattttata ttacttttta gtttgatact aagtattaaa catatttctg tattcttcca      402
aaaaaaaaaa a      413

<210> 148
<211> 609
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 139..231
<223> Von Heijne matrix
      score 4.40000009536743
      seq TCCHLGLPHPVRA/PR

<221> polyA_signal
<222> 579..584

<221> polyA_site
<222> 598..609

<400> 148
tgtcggagtt ggaaaggagc gacctgtttc cccccaagcg aaccgggatg ggaagtgact      60
tcaatgagat tgaacttcag ctggattgaa agagaggcta gaagtccgc ttgccagcag      120
cctccttagt agagcgga atg agt aat acc cac acg gtg ctt gtc tca ctt      171
                      Met Ser Asn Thr His Thr Val Leu Val Ser Leu
                      -30                      -25
ccc cat ccg cac ccg gcc ctc acc tgc tgt cac ctc ggc ctc cca cac      219

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Pro His Pro His Pro Ala Leu Thr Cys Cys His Leu Gly Leu Pro His	
-20 -15 -10 -5	
ccg gtc cgc gct ccc cgc cct ctt cct cgc gta gaa ccg tgg gat cct	267
Pro Val Arg Ala Pro Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro	
1 5 10	
agg tgg cag gac tca gag cta agg tat cca cag gcc atg aat tcc ttc	315
Arg Trp Gln Asp Ser Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe	
15 20 25	
cta aat gag cgg tca tcg ccg tgc agg acc tta agg caa gaa gca tcg	363
Leu Asn Glu Arg Ser Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser	
30 35 40	
gct gac aga tgt gat ctc tgaacctgat agattgctga ttttatctta	411
Ala Asp Arg Cys Asp Leu	
45 50	
ttttatcctt gacttggtac aagttttggg atttctgaaa agaccataca gataaccaca	471
aatatcaaga aagtcgtctt cagtattaag tagaatttag atttaggttt ccttcctgct	531
tcccacctcc ttcgaataag gaaacgtctt tgggaccaac tttatggaat aaataagctg	591
agctgcacaaa aaaaaaaaa	609

<210> 149
 <211> 522
 <212> DNA
 <213> Homo sapiens

<220>
 <221> polyA_site
 <222> 512..522

<400> 149

ccaactgcag nttcgaattt accgagcggg gaggagatgc acacggcact cgagtgtgag	60
gaaaaataga a atg aag gta cat atg cac aca aaa ttt tgc ctc att tgt	110
Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys	
1 5 10	
ttg ctg aca ttt att ttt cat cat tgc aac cat tgc cat gaa gaa cat	158
Leu Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His	
15 20 25	
gac cat ggc cct gaa gcg ctt cac aga cag cat cgt gga atg aca gaa	206
Asp His Gly Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu	
30 35 40 45	
ttg gag cca agc aaa ttt tca aag caa gct gct gaa aat gaa aaa aaa	254
Leu Glu Pro Ser Lys Phe Ser Lys Gln Ala Glu Asn Glu Lys Lys	
50 55 60	
tac tat att gaa aaa ctt ttt gag cgt tat ggt gaa aat gga aga tta	302
Tyr Tyr Ile Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu	
65 70 75	
tcc ttt ttt ggt ttg gag aaa ctt tta aca aac ttg ggc ctt gga gag	350
Ser Phe Phe Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu	
80 85 90	
aga aaa gta gtt gag att aat cat gag gat ctt ggc cac gat cat gtt	398
Arg Lys Val Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val	
95 100 105	
tct cat tta ggt att ttg gca gtt caa gag gga aag cat ttt cac tca	446
Ser His Leu Gly Ile Leu Ala Val Gln Glu Gly Lys His Phe His Ser	
110 115 120 125	
cat aac cac cag cat tcc cat aat cat tta aat tca gaa aat caa act	494
His Asn His Gln His Ser His Asn His Leu Asn Ser Glu Asn Gln Thr	
130 135 140	

gtg acc agt gta tcc aca aaaaaaaaaa
 Val Thr Ser Val Ser Thr
 145

522

<210> 150
 <211> 1322
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 126..260
 <223> Von Heijne matrix
 score 4.59999990463257
 seq VLVYLVTAERVWS/DD

<221> polyA_signal
 <222> 1283..1288

<221> polyA_site
 <222> 1309..1322

<400> 150
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 gctgctggga gccaggagag ccctgaggag tagtcaactca gtagcagctg acgcgtgggt 120
 ccacc atg aac tgg agt atc ttt gag gga ctc ctg agt ggg gtc aac aag 170
 Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys
 -45 -40 -35
 tac tcc aca gcc ttt ggg cgc atc tgg ctg tct ctg gtc ttc atc ttc 218
 Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe
 -30 -25 -20 -15
 cgc gtg ctg gtg tac ctg gtg acg gcc gag cgt gtg tgg agt gat gac 266
 Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp
 -10 -5 1
 cac aag gac ttc gac tgc aat act cgc cag ccc ggc tgc tcc aac gtc 314
 His Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val
 5 10 15
 tgc ttt gat gag ttc ttc cct gtg tcc cat gtg cgc ctc tgg gcc ctg 362
 Cys Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu
 20 25 30
 cag ctt atc ctg gtg aca tgc ccc tca ctg ctc gtg gtc atg cac gtg 410
 Gln Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val
 35 40 45 50
 gcc tac cgg gag gtt cag gag aag agg cac cga gaa gcc cat ggg gag 458
 Ala Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu
 55 60 65
 aac agt ggg cgc ctc tac ctg aac ccc ggc aag aag cgg ggt ggg ctc 506
 Asn Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu
 70 75 80
 tgg tgg aca tat gtc tgc agc cta gtg ttc aag gcg agc gtg gac atc 554
 Trp Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile
 85 90 95
 gcc ttt ctc tat gtg ttc cac tca ttc tac ccc aaa tat atc ctc cct 602
 Ala Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro
 100 105 110
 cct gtg gtc aag tgc cac gca gat cca tgt ccc aat ata gtg gac tgc 650
 Pro Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys

115	120	125	130	
ttc atc tcc aag ccc tca gag aag aac att ttc acc ctc ttc atg gtg				698
Phe Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val				
	135	140	145	
gcc aca gct gcc atc tgc atc ctg ctc aac ctc gtg gag ctc atc tac				746
Ala Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr				
	150	155	160	
ctg gtg agc aag aga tgc cac gag tgc ctg gca gca agg aaa gct caa				794
Leu Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln				
	165	170	175	
gcc atg tgc aca ggt cat cac ccc cac gat acc acc tct tcc tgc aaa				842
Ala Met Cys Thr Gly His His Pro His Asp Thr Thr Ser Ser Cys Lys				
	180	185	190	
caa gac gac ctc ctt tcg ggt gac ctc atc ttt ctg ggc tca gac agt				890
Gln Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser				
	195	200	205	210
cat cct cct ctc tta cca gac cgc ccc cga gac cat gtg aag aaa acc				938
His Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr				
	215	220	225	
atc ttg tgaggggctg cctggactgg tctggcaggt tgggcctgga tggggaggct				994
Ile Leu				
ctagcatctc tcataggtgc aacctgagag tgggggagct aagccatgag gtaggggcag				1054
gcaagagaga ggattcagac gctctgggag ccagttccta gtcctcaact ccagccacct				1114
gccccagctc gacggcactg ggccagttcc ccctctgctc tgcagctcgg tttccttttc				1174
tagaatggaa atagtgaggg ccaatgccca gggttggagg gaggagggcg ttcatagaag				1234
aacacacatg cgggcacctt catcgtgtgt ggcccactgt cagaacttaa taaaagtcaa				1294
ctcatttgct ggttaaaaaa aaaaaaaa				1322

<210> 151
 <211> 1290
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 50..160
 <223> Von Heijne matrix
 score 4
 seq PLSLDCGHS LCRA/CI
 <221> polyA_site
 <222> 1280..1290

<400> 151	
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	Met Ala Ser
	-35
aaa atc ttg ctt aac gta caa gag gag gtg acc tgt ccc atc tgc ctg	106
Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys Pro Ile Cys Leu	
	-30 -25 -20
gag ctg ttg aca gaa ccc ttg agt cta gac tgt ggc cac agc ctc tgc	154
Glu Leu Leu Thr Glu Pro Leu Ser Leu Asp Cys Gly His Ser Leu Cys	
	-15 -10 -5
cga gcc tgc atc act gtg agc aac aag gag gca gtg acc agc atg gga	202
Arg Ala Cys Ile Thr Val Ser Asn Lys Glu Ala Val Thr Ser Met Gly	
	1 5 10
gga aaa agc agc tgt cct gtg tgt ggt atc agt tac tca ttt gaa cat	250

Gly 15	Lys	Ser	Ser	Cys	Pro	Val	Cys	Gly	Ile	Ser	Tyr	Ser	Phe	Glu	His	
cta	cag	gct	aat	cag	cat	ctg	gcc	aac	ata	gtg	gag	aga	ctc	aag	gag	298
Leu	Gln	Ala	Asn	Gln	His	Leu	Ala	Asn	Ile	Val	Glu	Arg	Leu	Lys	Glu	
				35				40					45			
gtc	aag	ttg	agc	cca	gac	aat	ggg	aag	aag	aga	gat	ctc	tgt	gat	cat	346
Val	Lys	Leu	Ser	Pro	Asp	Asn	Gly	Lys	Lys	Arg	Asp	Leu	Cys	Asp	His	
			50					55				60				
cat	gga	gag	aaa	ctc	cta	ctc	ttc	tgt	aag	gag	gat	agg	aaa	gtc	att	394
His	Gly	Glu	Lys	Leu	Leu	Leu	Phe	Cys	Lys	Glu	Asp	Arg	Lys	Val	Ile	
			65				70					75				
tgc	tgg	ctt	tgt	gag	cgg	tct	cag	gag	cac	cgt	ggt	cac	cac	aca	gtc	442
Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	Glu	His	Arg	Gly	His	His	Thr	Val	
	80						85				90					
ctc	acg	gag	gaa	gta	ttc	aag	gaa	tgt	cag	gag	aaa	ctc	cag	gca	gtc	490
Leu	Thr	Glu	Glu	Val	Phe	Lys	Glu	Cys	Gln	Glu	Lys	Leu	Gln	Ala	Val	
	95				100				105						110	
ctc	aag	agg	ctg	aag	aag	gaa	gag	gag	gaa	gct	gag	aag	ctg	gaa	gct	538
Leu	Lys	Arg	Leu	Lys	Lys	Glu	Glu	Glu	Glu	Ala	Glu	Lys	Leu	Glu	Ala	
				115					120					125		
gac	atc	aga	gaa	gag	aaa	act	tcc	tgg	aag	tat	cag	gta	caa	act	gag	586
Asp	Ile	Arg	Glu	Glu	Lys	Thr	Ser	Trp	Lys	Tyr	Gln	Val	Gln	Thr	Glu	
			130					135					140			
aga	caa	agg	ata	caa	aca	gaa	ttt	gat	cag	ctt	aga	agc	atc	cta	aat	634
Arg	Gln	Arg	Ile	Gln	Thr	Glu	Phe	Asp	Gln	Leu	Arg	Ser	Ile	Leu	Asn	
			145				150					155				
aat	gag	gag	cag	aga	gag	ctg	caa	aga	ttg	gaa	gaa	gaa	gaa	aag	aag	682
Asn	Glu	Glu	Gln	Arg	Glu	Leu	Gln	Arg	Leu	Glu	Glu	Glu	Glu	Lys	Lys	
	160					165				170						
acg	ctg	gat	aag	ttt	gca	gag	gct	gag	gat	gag	cta	ggt	cag	cag	aag	730
Thr	Leu	Asp	Lys	Phe	Ala	Glu	Ala	Glu	Asp	Glu	Leu	Val	Gln	Gln	Lys	
	175				180					185					190	
cag	ttg	gtg	aga	gag	ctc	atc	tca	gat	gtg	gag	tgt	cgg	agt	cag	ttg	778
Gln	Leu	Val	Arg	Glu	Leu	Ile	Ser	Asp	Val	Glu	Cys	Arg	Ser	Gln	Trp	
				195					200					205		
tca	aca	atg	gag	ctg	ctg	cag	gac	atg	agt	gga	atc	atg	aaa	ttg	agt	826
Ser	Thr	Met	Glu	Leu	Leu	Gln	Asp	Met	Ser	Gly	Ile	Met	Lys	Trp	Ser	
			210				215						220			
gag	atc	tgg	agg	ctg	aaa	aag	cca	aaa	atg	ggt	tcc	aag	aaa	ctg	aag	874
Glu	Ile	Trp	Arg	Leu	Lys	Lys	Pro	Lys	Met	Val	Ser	Lys	Lys	Leu	Lys	
			225				230					235				
act	gta	ttc	cat	gct	cca	gat	ctg	agt	agg	atg	ctg	caa	atg	ttt	aga	922
Thr	Val	Phe	His	Ala	Pro	Asp	Leu	Ser	Arg	Met	Leu	Gln	Met	Phe	Arg	
			240			245					250					
gaa	ctg	aca	gct	gtc	cgg	tgc	tac	tgg	gtg	gat	gtc	aca	ctg	aat	tca	970
Glu	Leu	Thr	Ala	Val	Arg	Cys	Tyr	Trp	Val	Asp	Val	Thr	Leu	Asn	Ser	
	255				260					265					270	
gtc	aac	cta	aat	ttg	aat	ctt	gtc	ctt	tca	gaa	gat	cag	aga	caa	gtg	1018
Val	Asn	Leu	Asn	Leu	Asn	Leu	Val	Leu	Ser	Glu	Asp	Gln	Arg	Gln	Val	
				275						280				285		
ata	tct	gtg	cca	att	tgg	cct	ttt	cag	tgt	tat	aat	tat	ggt	gtc	ttg	1066
Ile	Ser	Val	Pro	Ile	Trp	Pro	Phe	Gln	Cys	Tyr	Asn	Tyr	Gly	Val	Leu	
			290				295						300			
gga	tcc	caa	tat	ttc	tcc	tct	ggg	aaa	cat	tac	tgg	gaa	gtg	gac	gtg	1114
Gly	Ser	Gln	Tyr	Phe	Ser	Ser	Gly	Lys	His	Tyr	Trp	Glu	Val	Asp	Val	
			305				310					315				
tcc	aag	aaa	act	gcc	tgg	atc	ctg	ggg	gta	tac	tgt	aga	aca	tat	tcc	1162
Ser	Lys	Lys	Thr	Ala	Trp	Ile	Leu	Gly	Val	Tyr	Cys	Arg	Thr	Tyr	Ser	

320	325	330	
cgc cat atg aag tat gtt gtt aga aga tgt gca aat cgt caa aat ctt			1210
Arg His Met Lys Tyr Val Val Arg Arg Cys Ala Asn Arg Gln Asn Leu			
335	340	345	350
tac acc aaa tac aga cct cta ttt ggc tac tgg gtt ata ggg tta cag			1258
Tyr Thr Lys Tyr Arg Pro Leu Phe Gly Tyr Trp Val Ile Gly Leu Gln			
355	360	365	
aat aaa tgt aag tat ggt gcc aaaaaaaaa a			1290
Asn Lys Cys Lys Tyr Gly Ala			
370			

<210> 152
 <211> 1364
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 83..139
 <223> Von Heijne matrix
 score 8.60000038146973
 seq LLWLALACSPVHT/TL

<221> polyA_site
 <222> 1356..1354

<400> 152

gcctgggagc tgaggcagcc accgtctcag cctggccagc cctctggacc ccgaggttgg	60
accctactgt gacacaccta cc atg cgg aca ctc ttc aac ctc ctc tgg ctt	112
Met Arg Thr Leu Phe Asn Leu Leu Trp Leu	
-15	-10
gcc ctg gcc tgc agc cct gtt cac act acc ctg tca aag tca gat gcc	160
Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala	
-5	1
aaa aaa gcc gcc tca aag acg ctg ctg gag aag agt cag ttt tca gat	208
Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp	
10	15
aag ccg gtg caa gac cgg ggt ttg gtg gtg acg gac ctc aaa gct gag	256
Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu	
25	30
agt gtg gtt ctt gag cat cgc agc tac tgc tgc gca aag gcc cgg gac	304
Ser Val Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp	
40	45
aga cac ttt gct ggg gat gta ctg ggc tat gtc act cca tgg aac agc	352
Arg His Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser	
60	65
cat ggc tac gat gtc acc aag gtc ttt ggg agc aag ttc aca cag atc	400
His Gly Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile	
75	80
tca ccc gtc tgg ctg cag ttg aag aga cgt ggc cgt gag atg ttt gag	448
Ser Pro Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu	
90	95
gtc acg ggc ctc cac gac gtg gac caa ggg tgg atg cga gct gtc agg	496
Val Thr Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg	
105	110
aag cat gcc aag ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac	544
Lys His Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp	
	115

120	125	130	135	
tgg act tac gat gat ttc cgg aac gtc tta gac agt gag gat gag ata				592
Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile				
	140	145	150	
gag gag ctg agc aag acc gtg gtc cag gtg gca aag aac cag cat ttc				640
Glu Glu Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe				
	155	160	165	
gat ggc ttc gtg gtg gag gtc tgg aac cag ctg cta agc cag aag cgc				688
Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg				
	170	175	180	
gtg ggc ctc atc cac atg ctc acc cac ttg gcc gag gcc ctg cac cag				736
Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln				
	185	190	195	
gcc cgg ctg ctg gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg				784
Ala Arg Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly				
	200	205	210	215
acc gac cag ctg ggc atg ttc acg cac aag gag ttt gag cag ctg gcc				832
Thr Asp Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala				
	220	225	230	
ccc gtg ctg gat ggt ttc agc ctc atg acc tac gac tac tct aca gcg				880
Pro Val Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala				
	235	240	245	
cat cag cct ggc cct aat gca ccc ctg tcc tgg gtt cga gcc tgc gtc				928
His Gln Pro Gly Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val				
	250	255	260	
cag gtc ctg gac ccg aag tcc aag tgg cga agc aaa atc ctc ctg ggg				976
Gln Val Leu Asp Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly				
	265	270	275	
ctc aac ttc tat ggt atg gac tac gcg acc tcc aag gat gcc cgt gag				1024
Leu Asn Phe Tyr Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu				
	280	285	290	295
cct gtt gtc ggg gcc agg tac atc cag aca ctg aag gac cac agg ccc				1072
Pro Val Val Gly Ala Arg Tyr Ile Gln Thr Leu Lys Asp His Arg Pro				
	300	305	310	
cgg atg gtg tgg gac agc cag gcc tca gag cac ttc ttc gag tac aag				1120
Arg Met Val Trp Asp Ser Gln Ala Ser Glu His Phe Phe Glu Tyr Lys				
	315	320	325	
aag agc cgc agt ggg agg cac gtc gtc ttc tac cca acc ctg aag tcc				1168
Lys Ser Arg Ser Gly Arg His Val Val Phe Tyr Pro Thr Leu Lys Ser				
	330	335	340	
ctg cag gtg cgg ctg gag ctg gcc cgg gag ctg ggc gtt ggg gtc tct				1216
Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly Val Gly Val Ser				
	345	350	355	
atc tgg gag ctg ggc cag ggc ctg gac tac ttc tac gac ctg ctc				1261
Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu				
	360	365	370	
taggtgggca ttgcggcctc cgcggtggac gtgttctttt ctaagccatg gagtgagtga				1321
gcaggtgtga aatacaggcc tccactccgt ttgcaaaaaa aaa				1364

<210> 153
 <211> 1470
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 57..95

<223> Von Heijne matrix
 score 3.90000009536743
 seq MLLSIGMLMLSAT/QV

<221> polyA_signal
 <222> 1438..1443

<221> polyA_site
 <222> 1458..1470

<400> 153

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gctggcaaga ctgtttgtgt tgcgggggcc ggacttcaag gtgattttac aacgag atg      59
                                     Met
ctg ctc tcc ata ggg atg ctc atg ctg tca gcc aca caa gtc tac acc      107
Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr Thr
-10                                -5                                1
gtc ttg act gtc cag ctc ttt gca ttc tta aac cca ctg cct gta gaa      155
Val Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Pro Leu Pro Val Glu
5                                10                                15                                20
gca gac att tta gca tat aac ttt gaa aat gca tct cag aca ttt gat      203
Ala Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe Asp
25                                30                                35
gac ctc cct gca aga ttt ggt tat aga ctt cca gct gaa ggt tta aag      251
Asp Leu Pro Ala Arg Phe Gly Tyr Arg Leu Pro Ala Glu Gly Leu Lys
40                                45                                50
ggg ttt tta att aac tca aaa cca gag aat gcc tgt gaa ccc ata gtg      299
Gly Phe Leu Ile Asn Ser Lys Pro Glu Asn Ala Cys Glu Pro Ile Val
55                                60                                65
cct cca cca gta aaa gac aat tca tct ggc act ttc atc gtg tta att      347
Pro Pro Pro Val Lys Asp Asn Ser Ser Gly Thr Phe Ile Val Leu Ile
70                                75                                80
aga aga ctt gat tgt aat ttt gat ata aag gtt tta aat gca cag aga      395
Arg Arg Leu Asp Cys Asn Phe Asp Ile Lys Val Leu Asn Ala Gln Arg
85                                90                                95                                100
gca gga tac aag gca gcc ata gtt cac aat gtt gat tct gat gac ctc      443
Ala Gly Tyr Lys Ala Ala Ile Val His Asn Val Asp Ser Asp Asp Leu
105                                110                                115
att agc atg gga tcc aac gac att gag gta cta aag aaa att gac att      491
Ile Ser Met Gly Ser Asn Asp Ile Glu Val Leu Lys Lys Ile Asp Ile
120                                125                                130
cca tct gtc ttt att ggt gaa tca tca gct agt tct ctg aaa gat gaa      539
Pro Ser Val Phe Ile Gly Glu Ser Ser Ala Ser Ser Leu Lys Asp Glu
135                                140                                145
ttc aca tat gaa aaa ggg ggc cac ctt atc tta gtt cca gaa ttt agt      587
Phe Thr Tyr Glu Lys Gly Gly His Leu Ile Leu Val Pro Glu Phe Ser
150                                155                                160
ctt cct ttg gaa tac tac cta att ccc ttc ctt atc ata gtg ggc atc      635
Leu Pro Leu Glu Tyr Tyr Leu Ile Pro Phe Leu Ile Ile Val Gly Ile
165                                170                                175                                180
tgt ctc atc ttg ata gtc att ttc atg atc aca aaa ttt gtc cag gat      683
Cys Leu Ile Leu Ile Val Ile Phe Met Ile Thr Lys Phe Val Gln Asp
185                                190                                195
aga cat aga gct aga aga aac aga ctt cgt aaa gat caa ctt aag aaa      731
Arg His Arg Ala Arg Arg Asn Arg Leu Arg Lys Asp Gln Leu Lys Lys
200                                205                                210
ctt cct gta cat aaa ttc aag aaa gga gat gag tat gat gta tgt gcc      779
Leu Pro Val His Lys Phe Lys Lys Gly Asp Glu Tyr Asp Val Cys Ala
215                                220                                225

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att tgt ttg gat gag tat gaa gat gga gac aaa ctc aga atc ctt ccc      827
Ile Cys Leu Asp Glu Tyr Glu Asp Gly Asp Lys Leu Arg Ile Leu Pro
 230                235                240
tgt tcc cat gct tat cat tgc aag tgt gta gac cct-tgg cta act aaa      875
Cys Ser His Ala Tyr His Cys Lys Cys Val Asp Pro Trp Leu Thr Lys
 245                250                255                260
acc aaa aaa acc tgt cca gtg tgc agg caa aaa gtt gtt cct tct caa      923
Thr Lys Lys Thr Cys Pro Val Cys Arg Gln Lys Val Val Pro Ser Gln
                265                270                275
ggc gat tca gac tct gac aca gac agt agt caa gaa gaa aat gaa gtg      971
Gly Asp Ser Asp Ser Asp Thr Asp Ser Ser Gln Glu Glu Asn Glu Val
                280                285                290
aca gaa cat acc cct tta ctg aga cct tta gct tct gtc agt gcc cag      1019
Thr Glu His Thr Pro Leu Leu Arg Pro Leu Ala Ser Val Ser Ala Gln
                295                300                305
tca ttt ggg gct tta tcg gaa tcc cgc tca cat cag aac atg aca gaa      1067
Ser Phe Gly Ala Leu Ser Glu Ser Arg Ser His Gln Asn Met Thr Glu
                310                315                320
tct tca gac tat gag gaa gac gac aat gaa gat act gac agt agt gat      1115
Ser Ser Asp Tyr Glu Glu Asp Asp Asn Glu Asp Thr Asp Ser Ser Asp
                325                330                335                340
gca gaa aat gaa att aat gaa cat gat gtc gtg gtc cag ttg cag cct      1163
Ala Glu Asn Glu Ile Asn Glu His Asp Val Val Val Gln Leu Gln Pro
                345                350                355
aat ggt gaa cgg gat tac aac ata gca aat act gtt tgactttcag      1209
Asn Gly Glu Arg Asp Tyr Asn Ile Ala Asn Thr Val
                360                365
aagatgattg gtttatttcc ctttaaaatg attaggtata tactgtaatt tgattttttg      1269
ctcccttaaa agatttctgt agaaataact tatttttttag tactctacag tttaatcaaa      1329
ttactgaaac aggacttttg atctggtatt tatctgccaa gaatatactt cattcactaa      1389
taatagactg gtgctgtaac tcaagcatca attcagctct tcttttgtaa tgaaagtata      1449
gccaaaacaa aaaaaaaaaa a      1470

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<210> 154
<211> 982
<212> DNA
<213> Homo sapiens

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<220>
<221> sig_peptide
<222> 72..197
<223> Von Heijne matrix
      score 7.19999980926514
      seq ILFSLSFLLVIIIT/FP

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<221> polyA_site
<222> 970..982

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<400> 154
gtgcctgtt cttcacactt agctccaaac ccatgaaaaa ttgccaagta taaaagcttc      60
tcaagaatga g atg gat tct agg gtg tct tca cct gag aag caa gat aaa      110
      Met Asp Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys
                -40                -35                -30
gag aat ttc gtg ggt gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg      158
Glu Asn Phe Val Gly Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp
                -25                -20                -15
atc ctg ttt tcc ctc tct ttc ctg ttg gtg atc att acc ttc ccc atc      206

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Ile	Leu	Phe	Ser	Leu	Ser	Phe	Leu	Leu	Val	Ile	Ile	Thr	Phe	Pro	Ile		
			-10				-5					1					
tcc	ata	tgg	atg	tgc	ttg	aag	atc	att	agg	gag	tat	gaa	cgt	gct	gtt	254	
Ser	Ile	Trp	Met	Cys	Leu	Lys	Ile	Ile	Arg	Glu	Tyr	Glu	Arg	Ala	Val		
5						10					15						
gta	ttc	cgt	ctg	gga	cgc	atc	caa	gct	gac	aaa	gcc	aag	ggg	cca	ggt	302	
Val	Phe	Arg	Leu	Gly	Arg	Ile	Gln	Ala	Asp	Lys	Ala	Lys	Gly	Pro	Gly		
20					25				30						35		
ttg	atc	ctg	gtc	ctg	cca	tgc	ata	gat	gtg	ttt	gtc	aag	gtt	gac	ctc	350	
Leu	Ile	Leu	Val	Leu	Pro	Cys	Ile	Asp	Val	Phe	Val	Lys	Val	Asp	Leu		
				40					45					50			
cga	aca	gtt	act	tgc	aac	att	cct	cca	caa	gag	atc	ctc	acc	aga	gac	398	
Arg	Thr	Val	Thr	Cys	Asn	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Arg	Asp		
			55					60					65				
tcc	gta	act	act	cag	gta	gat	gga	gtt	gtc	tat	tac	aga	atc	tat	agt	446	
Ser	Val	Thr	Thr	Gln	Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Ile	Tyr	Ser		
		70					75					80					
gct	gtc	tca	gca	gtg	gct	aat	gtc	aac	gat	gtc	cat	caa	gca	aca	ttt	494	
Ala	Val	Ser	Ala	Val	Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe		
		85				90					95						
ctg	ctg	gct	caa	acc	act	ctg	aga	aat	gtc	tta	ggg	aca	cag	acc	ttg	542	
Leu	Leu	Ala	Gln	Thr	Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Gln	Thr	Leu		
100					105					110					115		
tcc	cag	atc	tta	gct	gga	cga	gaa	gag	atc	gcc	cat	agc	atc	cag	act	590	
Ser	Gln	Ile	Leu	Ala	Gly	Arg	Glu	Glu	Ile	Ala	His	Ser	Ile	Gln	Thr		
				120					125					130			
tta	ctt	gat	gat	gcc	acc	gaa	ctg	tgg	ggg	atc	cgg	gtg	gcc	cga	gtg	638	
Leu	Leu	Asp	Asp	Ala	Thr	Glu	Leu	Trp	Gly	Ile	Arg	Val	Ala	Arg	Val		
		135					140					145					
gaa	atc	aaa	gat	gtt	cgg	att	ccc	gtg	cag	ttg	cag	aga	tcc	atg	gca	686	
Glu	Ile	Lys	Asp	Val	Arg	Ile	Pro	Val	Gln	Leu	Gln	Arg	Ser	Met	Ala		
		150					155					160					
gcc	gag	gct	gag	gcc	acc	cgg	gaa	gcg	aga	gcc	aag	gtc	ctt	gca	gct	734	
Ala	Glu	Ala	Glu	Ala	Thr	Arg	Glu	Ala	Arg	Ala	Lys	Val	Leu	Ala	Ala		
		165				170					175						
gaa	gga	gaa	atg	agt	gct	tcc	aaa	tcc	ctg	aag	tca	gcc	tcc	atg	gtg	782	
Glu	Gly	Glu	Met	Ser	Ala	Ser	Lys	Ser	Leu	Lys	Ser	Ala	Ser	Met	Val		
		180			185				190					195			
ctg	gct	gag	tct	ccc	ata	gct	ctc	cag	ctg	cgc	tac	ctg	cag	acc	ttg	830	
Leu	Ala	Glu	Ser	Pro	Ile	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	Gln	Thr	Leu		
				200					205					210			
agc	acg	gta	gcc	acc	gag	aag	aat	tct	acg	att	gtg	ttt	cct	ctg	ccc	878	
Ser	Thr	Val	Ala	Thr	Glu	Lys	Asn	Ser	Thr	Ile	Val	Phe	Pro	Leu	Pro		
		215						220				225					
atg	aat	ata	cta	gag	ggc	att	ggg	ggc	gtc	agc	tat	gat	aac	cac	aag	926	
Met	Asn	Ile	Leu	Glu	Gly	Ile	Gly	Gly	Val	Ser	Tyr	Asp	Asn	His	Lys		
		230				235					240						
aag	ctt	cca	aat	aaa	gcc	tgaggtcctc	ttgcggtagt	cagctaaaaa	aaaaaaaa							982	
Lys	Leu	Pro	Asn	Lys	Ala												
		245															

<210> 155

<211> 455

<212> DNA

<213> Homo sapiens

<220>

<221> polyA_signal
<222> 425..430

<221> polyA_site
<222> 443..455

<400> 155

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    1          5          10          15
gga acc tat ttg cct cag tcc tat ctg att cat gag cac atg gtt att      96
Gly Thr Tyr Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile
          20          25          30
act gat cgc atc gaa aac att gat cac ctg ggt ttc ttt att tat cga     144
Thr Asp Arg Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg
          35          40          45
ctg tgt cat gac aag gaa act tac aaa ctg caa cgc aga gaa act att     192
Leu Cys His Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile
          50          55          60
aaa ggt att cag aaa cgt gaa gcc agc aat tgt ttc gca att cgg cat     240
Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His
          65          70          75
ttt gaa aac aaa ttt gcc gtg gaa act tta att tgt tct tgaacagtca     289
Phe Glu Asn Lys Phe Ala Val Glu Thr Leu Ile Cys Ser
          80          85          90
agaaaaacat tattgaggaa aattaatatc acagcataac cccacccttt acattttgtg     349
cagtgattat tttttaaggt cttctttcat gtaagtagca aacagggctt tactatcttt     409
tcattctcatt aattcaatta aaaccattac cccaaaaaaa aaaaaa                455
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<210> 156

<211> 738

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 90..278

<223> Von Heijne matrix

score 3.5

seq GLVCAGLADMARF/AE

<221> polyA_signal

<222> 704..709

<221> polyA_site

<222> 724..738

<400> 156

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gggaaaagtg actagctccc ctctgttgtc agccagggac gagaacacag ccacgtcccc     60
accgcggtgc caacgatccc tcggcgggcg atg tcg gcc gcc ggt gcc cga ggc     113
                               Met Ser Ala Ala Gly Ala Arg Gly
                               -60
ctg cgg gcc acc tac cac cgg ctc ccc gat aaa gtg gag ctg atg ctg     161
Leu Arg Ala Thr Tyr His Arg Leu Pro Asp Lys Val Glu Leu Met Leu
-55          -50          -45          -40
ccc gag aaa ttg agg ccg ttg tac aac cat cca gca ggt ccc aga aca     209
Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro Arg Thr
```

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      -35      -30      -25
ggt ttc ttc tgg gct cca att atg aaa tgg ggg ttg gtg tgt gct gga      257
Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys Ala Gly
      -20      -15      -10
ttg gct gat atg gcc aga cct gca gaa aaa ctt agc aca gct caa tct      305
Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala Gln Ser
      -5      1      5
gct gtt ttg atg gct aca ggg ttt att tgg tca aga tac tca ctt gta      353
Ala Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser Leu Val
10      15      20      25
att att ccg aaa aat tgg agt ctg ttt gct gtt aat ttc ttt gtg ggg      401
Ile Ile Pro Lys Asn Trp Ser Leu Phe Ala Val Asn Phe Phe Val Gly
30      35      40
gca gca gga gcc tct cag ctt ttt cgt att tgg aga tat aac caa gaa      449
Ala Ala Gly Ala Ser Gln Leu Phe Arg Ile Trp Arg Tyr Asn Gln Glu
45      50      55
cta aaa gct aaa gca cac aaa taaaagagtt cctgatcacc tgaacaatct      500
Leu Lys Ala Lys Ala His Lys
60
agatgtggac aaaaccattg ggacctagtt tattattttgg ttattgataa agcaaagcta      560
actgtgtgtt tagaaggcac tgtaactggt agctagttct tgattcaata gaaaaatgca      620
gcaaactttt aataacagtc tctctacatg acttaaggaa cttatctatg gatattagta      680
acatttttct accatttgtc cgtaataaac catacttgct cgtaaaaaaa aaaaaaaa      738

<210> 157
<211> 649
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 88..147
<223> Von Heijne matrix
      score 12.3999996185303
      seq ALLLGALLGTAWA/RR

<221> polyA_signal
<222> 619..624

<221> polyA_site
<222> 637..649

<400> 157
ccaaagtgg agtccagcgg tttccagcgg cttggggccac ggcggcggcc ctgggagcag      60
aggaggagcg accccattac gctaaag atg aaa ggc tgg ggt tgg ctg gcc ctg      114
      Met Lys Gly Trp Gly Trp Leu Ala Leu
      -20      -15
ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat      162
Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
-10      -5      1      5
ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa      210
Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu
10      15      20
att gcc cag gtg gac ccc aag aag acc att cag atg gga tcc ttc cgg      258
Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg
25      30      35
atc aat cca gat ggc agc cag tca gtg gtg gag gta act gtt act gtt      306

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Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Thr Val Thr Val	
40 45 50	
ccc cca aac aaa gta gct cac tct ggc ttt gga tgaaattcga ctgottaaaa	359
Pro Pro Asn Lys Val Ala His Ser Gly Phe Gly	
55 60	
aggaccttgg tctaatagaa atgaagaaaa cagactcaga aaaaagattt ggctctgtct	419
catttggag aagctgcagg cttattcccc atgcacttgc ttcctggctg caaaccttaa	479
tactttgttt ctgctgtaga atttgttagc aaacaggag tcctgatcag cacccttctc	539
cacatccaca tgactggttt ttaatgtagc actgtggtat acatgcaaac atccgttcaa	599
aatctgagtc ggagctaaaa ataaaaaatg aaaaaacaaa aaaaaaaaaa	649

<210> 158
 <211> 714
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 33..92
 <223> Von Heijne matrix
 score 12.3999996185303
 seq ALLLGALLGTAWA/RR

<221> polyA_site
 <222> 703..714

<400> 158	
agcagaggtg gagcgacccc attacgctaa ag atg aaa ggc tgg ggt tgg ctg	53
Met Lys Gly Trp Gly Trp Leu	
-20 -15	
gcc ctg ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc	101
Ala Leu Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser	
-10 -5 1	
cag gat ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa	149
Gln Asp Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu	
5 10 15	
tgg gaa att gcc cag gtg gac ccc aag aag acc att cag atg gga tct	197
Trp Glu Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser	
20 25 30 35	
ttc cgg atc aat cca gat ggc agc cag tca gtg gtg gag gtg cct tat	245
Phe Arg Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Pro Tyr	
40 45 50	
gcc cgc tca gag gcc cac ctc aca gag ctg ctg gag gag ata tgt gac	293
Ala Arg Ser Glu Ala His Leu Thr Glu Leu Leu Glu Glu Ile Cys Asp	
55 60 65	
cgg atg aag gag tat ggg gaa cag att gat cct tcc acc cat cgc aag	341
Arg Met Lys Glu Tyr Gly Glu Gln Ile Asp Pro Ser Thr His Arg Lys	
70 75 80	
aac tac gta cgt gta gtg ggc cgg aat gga gaa tcc agt gaa ctg gac	389
Asn Tyr Val Arg Val Val Gly Arg Asn Gly Glu Ser Ser Glu Leu Asp	
85 90 95	
cta caa ggc atc cga atc gac tca gat att agc ggc acc ctc aag ttt	437
Leu Gln Gly Ile Arg Ile Asp Ser Asp Ile Ser Gly Thr Leu Lys Phe	
100 105 110 115	
gcg tgt ggg agc att gtg gag gaa tac gag gat gaa ctc att gaa ttc	485
Ala Cys Gly Ser Ile Val Glu Glu Tyr Glu Asp Glu Leu Ile Glu Phe	
120 125 130	

ttt tcc cga gag gct gac aat gtt aaa gac aaa ctt tgc agt aag cga	533
Phe Ser Arg Glu Ala Asp Asn Val Lys Asp Lys Leu Cys Ser Lys Arg	
135 140 145	
aca gat ctt tgt gac cat gcc ctg cac ata tcg cat gat gag cta	578
Thr Asp Leu Cys Asp His Ala Leu His Ile Ser His Asp Glu Leu	
150 155 160	
tgaaccactg gagcagccca cactggcttg atggatcacc cccaggaggg gaaaatggtg	638
gcaatgcctt ttatatatta tgtttttact gaaattaact gaaaaaatat gaaacaaaa	698
gtacaaaaaa aaaaaa	714

<210> 159
 <211> 596
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 33..107
 <223> Von Heijne matrix
 score 5
 seq MFAASLLAMCAGA/EV

<221> polyA_signal
 <222> 546..551

<221> polyA_site
 <222> 584..596

<400> 159	
cacagttcct ctctctcctag agcctgccga cc atg ccc gcg ggc gtg ccc atg	53
Met Pro Ala Gly Val Pro Met	
-25 -20	
ttcc acc tac ctg aaa atg ttc gca gcc agt ctc ctg gcc atg tgc gca	101
Ser Thr Tyr Leu Lys Met Phe Ala Ala Ser Leu Leu Ala Met Cys Ala	
-15 -10 -5	
ggg gca gaa gtg gtg cac agg tac tac cga ccg gac ctg aca ata cct	149
Gly Ala Glu Val Val His Arg Tyr Tyr Arg Pro Asp Leu Thr Ile Pro	
1 5 10	
gaa att cca cca aag cgt gga gaa ctc aaa acg gag ctt ttg gga ctg	197
Glu Ile Pro Pro Lys Arg Gly Glu Leu Lys Thr Glu Leu Leu Gly Leu	
15 20 25 30	
aaa gaa aga aaa cac aaa cct caa gtt tct caa cag gag gaa ctt aaa	245
Lys Glu Arg Lys His Lys Pro Gln Val Ser Gln Gln Glu Glu Leu Lys	
35 40 45	
taactatgcc aagaattctg tgaataatat aagtcttaaa tatgtatttc ttaatttatt	305
gcatcaaact acttgtcctt aagcacttag tctaattgcta actgcaagag gaggtgctca	365
gtggatgttt agccgatacg ttgaaattta attacggttt gattgatatt tcttgaaaac	425
tgccaaagca catatcatca aaccatttca tgaatatggt ttggaagatg tttagtcttg	485
aatataacgc gaaatagaat atttgtaagt ctactatatg gggtgtcttt atttcatata	545
aattaagaaa ttattttaaaa ctatgaacta gtttcattaa aaaaaaaga a	596

<210> 160
 <211> 403
 <212> DNA
 <213> Homo sapiens

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<220>
<221> polyA_signal
<222> 375..380

<221> polyA_site
<222> 390..403

<400> 160
tgaagagaat ggctgttgca gtcggcgctca gagcagctcc agtgccgggg attcggacgg      60
agagcgcgag gactcggcgg ctgagcgcgc cgcacagcag ctagaggcgc tgctcaacaa      120
gact atg cgc att cgc atg aca gat gga cgg aca ctg gtc ggc tgc ttt      169
    Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe
      1         5         10         15
ctc tgc act gac cgt gac tgc aat gtc atc ctg ggc tcg gcg cag gag      217
Leu Cys Thr Asp Arg Asp Cys Asn Val Ile Leu Gly Ser Ala Gln Glu
      20         25         30
ttc ctc aag ccg tcg gat tcc ttc tct gcc ggg gag ccc cgt gtg ctg      265
Phe Leu Lys Pro Ser Asp Ser Phe Ser Ala Gly Glu Pro Arg Val Leu
      35         40         45
ggc ctg gcc atg gta ccc gga cac cac atc gtt tcc att gag gtg cag      313
Gly Leu Ala Met Val Pro Gly His His Ile Val Ser Ile Glu Val Gln
      50         55         60
agg gag agt ctg acc ggg cct ccg tat ctc tgaccacgat ggcgcttacc      363
Arg Glu Ser Leu Thr Gly Pro Pro Tyr Leu
      65         70
tttcagactt cattaaactt atgaccaaaaa aaaaaaaaaa      403

<210> 161
<211> 727
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 126..575
<223> Von Heijne matrix
      score 8.60000038146973
      seq LELLTSCSPPASASQ

<221> polyA_signal
<222> 670..675

<221> polyA_site
<222> 721..727

<400> 161
ctcagaactg tgctgggaag gatggtaggg cgactggggc tcacctccgc accgttgtag      60
gaccgggggt agggttttga gcccggtgga gctgccccac gcggcctcgt cctgccaacg      120
gtcgg atg gcg gag acg aag gac aca gcg cag atg ttg gtg acc ttc aag      170
    Met Ala Glu Thr Lys Asp Thr Ala Gln Met Leu Val Thr Phe Lys
      -150         -145         -140
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg      218
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
      -135         -130         -125         -120
gcc cag agg acc ctg tac cga gag ggc atc ggg ttc ccn aaa cca gag      266
Ala Gln Arg Thr Leu Tyr Arg Glu Gly Ile Gly Phe Pro Lys Pro Glu
      -115         -110         -105

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ttg gtc cac ctg cta gag cat ggg cag gag ctg tgg ata gtg aag aga      314
Leu Val His Leu Leu Glu His Gly Gln Glu Leu Trp Ile Val Lys Arg
      -100                      -95                      -90
ggc ctc tca cat gct acc tgt gca gag ttt cac tct tgt tgc cca ggc      362
Gly Leu Ser His Ala Thr Cys Ala Glu Phe His Ser Cys Cys Pro Gly
      -85                      -80                      -75
tgg agt gca gtg gnn cgc cat ctc agc tca ctg caa ctt ctg cct ccc      410
Trp Ser Ala Val Xaa Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro
      -70                      -65                      -60
gag ttc aag gga ttc tcc tgc ctc agc ctc ccg agt agc tgg gat tac      458
Glu Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr
      -55                      -50                      -45                      -40
agg cgc cca cca cca tgc ccg gct ggt ttt ttt gta ttt tta gta gag      506
Arg Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu
      -35                      -30                      -25
acg ggg ctt cac cat gtt ggc cag gct ggt ctt gaa ctc ttg acc tca      554
Thr Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser
      -20                      -15                      -10
tgt agt cca ccc gcc tct gcc tcc caa agt gct gcg att aca ggc gtg      602
Cys Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val
      -5                      1                      5
agc cac cgt gcc cgg cag aga aaa act gct taagggttgaa aagagaaatt      652
Ser His Arg Ala Arg Gln Arg Lys Thr Ala
10                      15
taagaaattg ctgacggaat aaaaacataa tagaactaca acaccgaagg aaatgaaaga      712
agcaaaaaaaaa aaaaaa      727

<210> 162
<211> 944
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 90..155
<223> Von Heijne matrix
      score 5.90000009536743
      seq IILGCLALFLLLQ/RK

<221> polyA_signal
<222> 913..918

<221> polyA_site
<222> 932..944

<400> 162
gaatcaggtt ccgtagccca cagaaaagaa gcaagggacg gcaggactgt ttcacacttt      60
tctgcttctg gaagtgctg gacaaaaaac atg gaa cta att tcc cca aca gtg      113
                      Met Glu Leu Ile Ser Pro Thr Val
                      -20                      -15
att ata atc ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag      161
Ile Ile Ile Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys
      -10                      -5                      1
aat ttg cgt aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga      209
Asn Leu Arg Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly
      5                      10                      15
gtt gga ttt gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca      257

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tgacgccatc aaggatgtct tggttctctg ttccttcttc ttggttcagg cttctgattg 470
tcctcaggct ggctcctcat agggatgctg ggtgctgcag ccttgactgg ggcagcaggc 530
cccatgttc aatccatcct cccaccttg aataaatgct ttcttttcac aatgagaaaa 590
aaaaaaaaa 598

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<210> 164
<211> 360
<212> DNA
<213> Homo sapiens

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<220>
<221> sig_peptide
<222> 85..150
<223> Von Heijne matrix
      score 5.90000009536743
      seq IILGCLALFLLQ/RK

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<221> polyA_site
<222> 349..360

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<400> 164
caggttccgt agccacagaa aagaagcaag ggacggcagg actgtttcac acttttctgc 60
ttctggaagg tgctggacaa aaac atg gaa cta att tcc cca aca gtg att 111
                               Met Glu Leu Ile Ser Pro Thr Val Ile
                               -20                               -15
ata atc ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat 159
Ile Ile Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn
      -10                               -5                               1
ttg cgt aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt 207
Leu Arg Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val
      5                               10                               15
gga ttt gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga 255
Gly Phe Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg
      20                               25                               30                               35
atc aag tat gga cca ata ttt aca gtc ttt gct atg gga aac cga atg 303
Ile Lys Tyr Gly Pro Ile Phe Thr Val Phe Ala Met Gly Asn Arg Met
      40                               45                               50
acc ttt gtt act gaa gaa gaa gga att aat gtg ttt cta aaa tcc 348
Thr Phe Val Thr Glu Glu Glu Gly Ile Asn Val Phe Leu Lys Ser
      55                               60                               65
aaaaaaaaaa aa 360

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<210> 165
<211> 490
<212> DNA
<213> Homo sapiens

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<220>
<221> sig_peptide
<222> 77..124
<223> Von Heijne matrix
      score 4.80000019073486
      seq SLFIYIFLTCSNT/SP

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<221> polyA_signal
<222> 461..466

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<221> polyA_site
 <222> 477..490

<400> 165

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atgagcttcc agccccaaga gtggaggctg ccacatccca acatagtatc tattgaaaag      60
gaagcagtgt gtatct atg att ata tct ctg ttc atc tat ata ttt ttg aca      112
                Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr
                -15                -10                -5
tgt agc aac acc tct cca tct tat caa gga act caa ctc ggt ctg ggt      160
Cys Ser Asn Thr Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly
                1                5                10
ctc ccc agt gcc cag tgg tgg cct ttg aca ggt agg agg atg cag tgc      208
Leu Pro Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys
                15                20                25
tgc agg cta ttt tgt ttt ttg tta caa aac tgt ctt ttc cct ttt ccc      256
Cys Arg Leu Phe Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro
                30                35                40
ctc cac ctg att cag cat gat ccc tgt gag ctg gtt ctc aca atc tcc      304
Leu His Leu Ile Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser
                45                50                55                60
tgg gac tgg gct gag gca ggg gct tcg ctc tat tct ccc taaccatact      353
Trp Asp Trp Ala Glu Ala Gly Ala Ser Leu Tyr Ser Pro
                65                70
gttttctttt ccccttgcc acttagcagt tatcccccca gctatgcctt ctccctccct      413
cccttgccct ggcataatatt gtgccttatt tatgctgcaa atataacatt aaactatcaa      473
gtgaaaaaaaa aaaaaaa      490
  
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<210> 166

<211> 488

<212> DNA

<213> Homo sapiens

<220>

<221> polyA_signal

<222> 458..463

<221> polyA_site

<222> 475..488

<400> 166

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ccgcttccga aaagagacag acaatgcagc catcata atg aag gtg gac aaa gac      55
                Met Lys Val Asp Lys Asp
                1                5
cgg cag atg gtg gtg ctg gag gaa gaa ttt cgg aac att tcc cca gag      103
Arg Gln Met Val Val Leu Glu Glu Glu Phe Arg Asn Ile Ser Pro Glu
                10                15                20
gag ctc aaa atg gag ttg ccg gag aga cag ccc agg ttc gtg gtt tac      151
Glu Leu Lys Met Glu Leu Pro Glu Arg Gln Pro Arg Phe Val Val Tyr
                25                30                35
agc tac aag tac gtg cgt gac gat ggc cga gtg tcc tac cct ttg tgt      199
Ser Tyr Lys Tyr Val Arg Asp Asp Gly Arg Val Ser Tyr Pro Leu Cys
                40                45                50
ttc atc ttc tcc agc cct gtg ggc tgc aag ccg gaa caa cag atg atg      247
Phe Ile Phe Ser Ser Pro Val Gly Cys Lys Pro Glu Gln Gln Met Met
                55                60                65                70
tat gca ggg agt aaa aac agg ctg gtg cag aca gca gag ctc aca aag      295
  
```

Tyr Ala Gly Ser Lys Asn Arg Leu Val Gln Thr Ala Glu Leu Thr Lys	
75 80 85	
gtg ttc gaa atc cgc acc act gat gac ctc act gag gcc tgg ctc caa	343
Val Phe Glu Ile Arg Thr Thr Asp Asp Leu Thr Glu Ala Trp Leu Gln	
90 95 100	
gaa aag ttg tct ttc ttt cgt tgatctctgg gctggggact gaattcctga	394
Glu Lys Leu Ser Phe Phe Arg	
105	
tgtctgagtc ctcaaggtga ctggggactt ggaaccccta ggacctgaac aaccaagact	454
ttaaataaat tttaaaatgc aaaaaaaaaa aaaa	488

<210> 167
 <211> 771
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 48..356
 <223> Von Heijne matrix
 score 4.90000009536743
 seq VYAFLGLTAPSGS/KE

<221> polyA_signal
 <222> 742..747
 <221> polyA_site
 <222> 760..771

<400> 167	
ccacagccct tttcaggacc caaacaaccg cagccgctgt tcccagg atg gtg atc	56
Met Val Ile	
cgt gta tat att gca tct tcc tct ggc tct aca gcg att aag aag aaa	104
Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile Lys Lys Lys	
-100 -95 -90 -85	
caa caa gat gtg ctt ggt ttc cta gaa gcc aac aaa ata gga ttt gaa	152
Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile Gly Phe Glu	
-80 -75 -70	
gaa aaa gat att gca gcc aat gaa gag aat cgg aag tgg atg aga gaa	200
Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp Met Arg Glu	
-65 -60 -55	
aat gta cct gag aat agt cga cca gcc aca ggt aac ccc ctg cca cct	248
Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Asn Pro Leu Pro Pro	
-50 -45 -40	
cag att ttc aat gaa agc cag tat cgc ggg gac tat gat gcc ttc ttt	296
Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr Asp Ala Phe Phe	
-35 -30 -25	
gaa gcc aga gaa aat aat gca gtg tat gcc ttc tta ggc ttg aca gcc	344
Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu Gly Leu Thr Ala	
-20 -15 -10 -5	
cca tct ggt tca aag gaa gca gaa gtg caa gca aag cag caa gca	389
Pro Ser Gly Ser Lys Glu Ala Glu Val Gln Ala Lys Gln Gln Ala	
1 5 10	
tgaacottga gcaactgtgct ttaagcatcc tgaaaaatga gtctccattg cttttataaa	449
atagcagaat tagctttgct tcaaaagaaa taggcttaat gttgaaataa tagattagtt	509
gggttttcac atgcaaacac tcaaaatgaa tacaaaatta aaatttgaac attatggtga	569
ttatggtgag gagaatggga tattaacata aaattatatt aataagtaga tatcgtagaa	629

atagtgttgt	tacctgccaa	gccatcctgt	atacaccaat	gattttacaa	agaaaacacc	689
cttccctcct	tctgccatta	ctatggcaac	ctaagtgtat	ctgcagctct	acattaaaaa	749
ggagaaagag	aaaaaaaaaa	aa				771

<210> 168
 <211> 959
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 69..359
 <223> Von Heijne matrix
 score 4
 seq RLPLVVSFIASSS/AN

<221> polyA_signal
 <222> 927..932

<221> polyA_site
 <222> 947..959

<400> 168	
cgagagagaac caggcagccc agaaacccca ggcgtggaga ttgatcctgc gagagaaggg	60
ggttcacatc atg gcg gat gac cta aag cga ttc ttg tat aaa aag tta cca	110
Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro	
-95 -90 -85	
agt gtt gaa ggg ctc cat gcc att gtt gtg tca gat aga gat gga gta	158
Ser Val Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val	
-80 -75 -70	
cct gtt att aaa gtg gca aat gac aat gct cca gag cat gct ttg cga	206
Pro Val Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg	
-65 -60 -55	
cct ggt ttc tta tcc act ttt gcc ctt gca aca gac caa gga agc aaa	254
Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys	
-50 -45 -40	
ctt gga ctt tcc aaa aat aaa agt atc atc tgt tac tat aac acc tac	302
Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr	
-35 -30 -25 -20	
cag gtg gtt caa ttt aat cgt tta cct ttg gtg gtg agt ttc ata gcc	350
Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala	
-15 -10 -5	
agc agc agt gcc aat aca gga cta att gtc agc cta gaa aag gaa ctt	398
Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu	
1 5 10	
gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa gtt tct	440
Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser	
15 20 25	
taatctgaca gtggtttcag tgtgtacctt atcttcatta taacaacaca atatcaatcc	500
agcaatcttt agactacaat aatactttta tccatgtgct caagaaaggg cccctttttc	560
caacttatac taaagagcta gcatatagat gtaatttata gatagatcag ttgctatatt	620
ttctgggtga gggcttttct tatttagtga gatctagggg taccacagaa atgggttcagt	680
ctatcacagc tcccatggag ttagtctggg caccagatat ggatgagaga ttctattcag	740
tgatcagaa tcaaactggg acattgatcc acttgagccg ttaagtgtg ccaattgtac	800
aatatgccca ggcttgca ataaagccaa ctttttattg tgaataataa taaggacata	860
tttttcttca gattatgttt tatttctttg cattgagtga ggaacataaa atggcttggt	920
aaaagtaata aaatcagtac aatcactaaa aaaaaaaaaa	959

<210> 169
 <211> 464
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 33..98
 <223> Von Heijne matrix
 score 9.80000019073486
 seq LVVFLALQLVPG/SP

<221> polyA_signal
 <222> 437..442

<221> polyA_site
 <222> 455..464

<400> 169

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gccagaactt actcaccat cccactgaca cc atg aag cct gtg ctg cct ctc      53
                                Met Lys Pro Val Leu Pro Leu
                                -20
cag ttc ctg gtg gtg ttc tgc cta gca ctg cag ctg gtg cct ggg agt      101
Gln Phe Leu Val Val Phe Cys Leu Ala Leu Gln Leu Val Pro Gly Ser
-15                                -10                                -5                                1
ccc aag cag cgt gtt ctg aag tat atc ttg gaa cct cca ccc tgc ata      149
Pro Lys Gln Arg Val Leu Lys Tyr Ile Leu Glu Pro Pro Pro Cys Ile
                                5                                10                                15
tca gca cct gaa aac tgt act cac ctg tgt aca atg cag gaa gat tgc      197
Ser Ala Pro Glu Asn Cys Thr His Leu Cys Thr Met Gln Glu Asp Cys
                                20                                25                                30
gag aaa gga ttt cag tgc tgt tcc tcc ttc tgt ggg ata gtc tgt tca      245
Glu Lys Gly Phe Gln Cys Cys Ser Ser Phe Cys Gly Ile Val Cys Ser
                                35                                40                                45
tca gaa aca ttt caa aag cgc aac aga atc aaa cac aag ggc tca gaa      293
Ser Glu Thr Phe Gln Lys Arg Asn Arg Ile Lys His Lys Gly Ser Glu
50                                55                                60                                65
gtc atc atg cct gcc aac tgaggcatat ttcttagatc attttgcctc      341
Val Ile Met Pro Ala Asn
                                70
tacgatgttt tttcttggtc cacctttagg aaggtattga gaagcaagaa actggaggcc      401
caatatctaa cctgcaaadc gtttttgagt ttggcaataa aggctaactc accaaaaaaa      461
aaa                                                                464

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<210> 170
 <211> 799
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 110..235
 <223> Von Heijne matrix
 score 5.19999980926514
 seq LLFDLVCHEFCQS/DD

<221> polyA_signal

<222> 764..769

<221> polyA_site

<222> 787..799

<400> 170

ccaacccag gaagagtctg aagagcagcc agtgtttcgg cttgtgccct gtatacttga 60
agctgccaaa caagtacgtt ctgaaaatcc agaatggctt gatgtttac atg cac att 118
Met His Ile

-40
tta caa ctg ctt act aca gtg gat gat gga att caa gca att gta cat 166
Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His

-35 -25
tgt cct gac act gga aaa gac att tgg aat cta ctt ttt gac ctg gtc 214
Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val

-20 -15 -10
tgc cat gaa ttc tgc cag tct gat gat cca ccc atc att ctt caa gaa 262
Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile Leu Gln Glu

-5 1 5
cag aaa aca gtg cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat 310
Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr

10 15 20 25
gcc tca cag act gag caa gag tat cta aag ata gaa aaa gta gat ctt 358
Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val Asp Leu

30 35 40
cct cta att gac agc ctc att cgg gtc tta caa aat atg gaa cag tgt 406
Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met Glu Gln Cys

45 50 55
cag aaa aaa cca gag aac tcg gca gag tct aac aca gag gaa act aaa 454
Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu Glu Thr Lys

60 65 70
agg act gat tta acc caa gat gat ttc cac ttg aaa atc tta aag gat 502
Arg Thr Asp Leu Thr Gln Asp Asp Phe His Leu Lys Ile Leu Lys Asp

75 80 85
att tta tgt gaa ttt ctt tct aat att ttt cag gca tta aca aag gag 550
Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu Thr Lys Glu

90 95 100 105
acg gtg gct cag gga gta aag gaa ggc cag ttg agc aaa cag aag tgt 598
Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys Gln Lys Cys

110 115 120
tcc tct gca ttt caa aac ctt ctt cct ttc tat agc cct gtg gtg gaa 646
Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro Val Val Glu

125 130 135
gat ttt att aaa atc cta cgt gaa gtt gat aag gcg ctt gct gat gac 694
Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu Ala Asp Asp

140 145 150
ttg gaa aaa aac ttc cca agt ttg aag gtt cag act taaaacctga 740
Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr

155 160 165
attggaatta cttctgtaca agaaataaac tttatttttc tcaactgaaaa aaaaaaaaaa 799

<210> 171

<211> 320

<212> DNA

<213> Homo sapiens

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<220>
<221> polyA_site
<222> 308..320

<400> 171
tcattcatcca gagcagccag tgtccgggag gcagaag atg ccc cac tcc aag cct      55
                                   Met Pro His Ser Lys Pro
                                   1       5
ctg gac tgg ggg ctc tct tca gtg gct gaa tgt cca gca gag cta ttt      103
Leu Asp Trp Gly Leu Ser Ser Val Ala Glu Cys Pro Ala Glu Leu Phe
      10       15       20
cct tcc aca ggg ggc ctt gca ggg aag ggt cca gga ctt gac atc tta      151
Pro Ser Thr Gly Gly Leu Ala Gly Lys Gly Pro Gly Leu Asp Ile Leu
      25       30       35
aga tgc gtc ttg tcc cct tgg gcc agt cat ttc ccc tct ctg agc ctc      199
Arg Cys Val Leu Ser Pro Trp Ala Ser His Phe Pro Ser Leu Ser Leu
      40       45       50
ggg gtc ttc aac ctg tgaaatggga tcataatcac tgccttacct ccctcacggt      254
Gly Val Phe Asn Leu
55
tggtgtgagg actgagtgtg tggaagtttt tcataaactt tggatgctag tgtaaaaaaa      314
aaaaaa      320

<210> 172
<211> 331
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 129..209
<223> Von Heijne matrix
      score 4.90000009536743
      seq CLLSYIALGAIHA/KI

<221> polyA_site
<222> 318..331

<400> 172
atggaaacca gatggggcaa cgggggtggtt ctagtgcaga ctgtagctgc agctcctctc      60
cacctctagc ctgctcatTT ccagctcaga aattctacta atggcgTTTT ttcttcctga      120
aaaaggaa atg aac agg gtc cct gct gat tct cca aat atg tgt cta atc      170
      Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile
      -25       -20       -15
tgt tta ctg agt tac ata gca ctt gga gcc atc cat gca aaa atc tgt      218
Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys
      -10       -5       1
agg aga gca ttc cag gaa gag gga aga gca aat gca aag acg ggc gtg      266
Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val
      5       10       15
aga gct tgg tgc ata cag cca tgg gcc aaa taaagtttcc ttggaatagc      316
Arg Ala Trp Cys Ile Gln Pro Trp Ala Lys
20       25
caaaaaaaaa aaaaaa      331

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<210> 173
 <211> 1075
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 78..359
 <223> Von Heijne matrix
 score 4.19999980926514
 seq IILTAVYFALSIS/LH

<221> polyA_signal
 <222> 1042..1047

<221> polyA_site
 <222> 1063..1075

<400> 173

gtggtagggg	gcagccagga	gcggttttct	gggaactgtg	ggatgtgcc	ttgggggcc	60
gagaaaacag	aaggaag	atg ctc cag acc agt aac tac agc ctg gtg ctc				110
		Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu				
		-90		-85		
tct ctg cag ttc ctg ctg ctg tcc tat gac ctc ttt gtc aat tcc ttc						158
Ser Leu Gln Phe Leu Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe						
		-80		-75		
tca gaa ctg ctc caa aag act cct gtc atc cag ctt gtg ctc ttc atc						206
Ser Glu Leu Leu Gln Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile						
		-65		-60		
atc cag gat att gca gtc ctc ttc aac atc atc atc att ttc ctc atg						254
Ile Gln Asp Ile Ala Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met						
		-50		-45		
ttc ttc aac acc ttc gtc ttc cag gct ggc ctg gtc aac ctc cta ttc						302
Phe Phe Asn Thr Phe Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe						
		-35		-30		
cat aag ttc aaa ggg acc atc atc ctg aca gct gtg tac ttt gcc ctc						350
His Lys Phe Lys Gly Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu						
		-15		-10		
agc atc tcc ctt cat gtc tgg gtc atg aac tta cgc tgg aaa aac tcc						398
Ser Ile Ser Leu His Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser						
		1		5		
aac agc ttc ata tgg aca gat gga ctt caa atg ctg ttt gta ttc cag						446
Asn Ser Phe Ile Trp Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln						
		15		20		
aga cta gca gca gtg ttg tac tgc tac ttc tat aaa cgg aca gcc gta						494
Arg Leu Ala Ala Val Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val						
		30		35		
aga cta ggc gat cct cac ttc tac cag gac tct ttg tgg ctg cgc aag						542
Arg Leu Gly Asp Pro His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys						
		50		55		
gag ttc atg caa gtt cga agg tgacctcttg tcacactgat ggatactttt						593
Glu Phe Met Gln Val Arg Arg						
		65				
ccttcctgat agaagccaca tttgctgctt tgcagggaga gttggcccta tgcattggca						653
aacagctgga ctttccaagg aaggttcaga ctagctgtgt tcagcattca agaaggaaga						713
tccccctct tgacaaatta gagggtcccc atcggtctcc agtgccgcat cccttccttg						773
ccttctacct ctgttcacc cccttccttc ctctcctctc tgtaccattc attctccctg						833
accggccttt cttgccgagg gttctgtggc tcttaccctt gtgaagcttt tcctttagcc						893

tgggacagaa	ggacctcccg	gcccccaaag	gatctcccag	tgaccaaagg	atgcgaagag	953
tgatagttac	gtgctcctga	ctgatcacac	cgcagacatt	tagattttta	tacccaaggc	1013
actttaaaaa	aatgttttat	aaatagagaa	taaattgaat	tcttgttcca	aaaaaaaaaa	1073
aa						1075

<210> 174
 <211> 632
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 62..265
 <223> Von Heijne matrix
 score 4.59999990463257
 seq LPFSLVSMMLVTQG/LV

<221> polyA_signal
 <222> 602..607

<221> polyA_site
 <222> 621..632

<400> 174

cactgggtca	aggagtaagc	agaggataaa	caactggaag	gagagcaagc	acaaagtc	cat	60
c atg gct tca gcg tct gct cgt gga aac caa gat aaa gat gcc cat ttt							109
Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe							
-65		-60		-55			
cca cca cca agc aag cag agc ctg ttg ttt tgt cca aaa tca aaa ctg							157
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu							
-50		-45		-40			
cac atc cac aga gca gag atc tca aag att atg cga gaa tgt cag gaa							205
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu							
-35		-30		-25			
gaa agt ttc tgg aag aga gct ctg cct ttt tct ctt gta agc atg ctt							253
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu							
-20		-15		-10		-5	
gtc acc cag gga cta gtc tac caa ggt tat ttg gca gct aat tct aga							301
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg							
1		5		10			
ttt gga tca ttg ccc aaa gtt gca ctt gct ggt ctc ttg gga ttt ggc							349
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly							
15		20		25			
ctt gga aag gta tca tac ata gga gta tgc cag agt aaa ttc cat ttt							397
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe							
30		35		40			
ttt gaa gat cag ctc cgt ggg gct ggt ttt ggt cca cag cat aac agg							445
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His Asn Arg							
45		50		55		60	
cac tgc ctc ctt acc tgt gag gaa tgc aaa ata aag cat gga tta agt							493
His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly Leu Ser							
65		70		75			
gag aag gga gac tct cag cct tca gct tcc taaattctgt gtctgtgact							543
Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser							
80		85					
ttcgaagttt	tttaaacctc	tgaatttgta	cacatttaaa	atttcaagtg	tactttaaaa		603
taaaatactt	ctaattgtaaa	aaaaaaaaaa					632

number	sex	condition	length	weight	age	year	month	day
1	♂	immature	110	10	1	1900	1	1
2	♂	immature	110	10	1	1900	1	1
3	♂	immature	110	10	1	1900	1	1
4	♂	immature	110	10	1	1900	1	1
5	♂	immature	110	10	1	1900	1	1
6	♂	immature	110	10	1	1900	1	1
7	♂	immature	110	10	1	1900	1	1
8	♂	immature	110	10	1	1900	1	1
9	♂	immature	110	10	1	1900	1	1
10	♂	immature	110	10	1	1900	1	1
11	♂	immature	110	10	1	1900	1	1
12	♂	immature	110	10	1	1900	1	1
13	♂	immature	110	10	1	1900	1	1
14	♂	immature	110	10	1	1900	1	1
15	♂	immature	110	10	1	1900	1	1
16	♂	immature	110	10	1	1900	1	1
17	♂	immature	110	10	1	1900	1	1
18	♂	immature	110	10	1	1900	1	1
19	♂	immature	110	10	1	1900	1	1
20	♂	immature	110	10	1	1900	1	1
21	♂	immature	110	10	1	1900	1	1
22	♂	immature	110	10	1	1900	1	1
23	♂	immature	110	10	1	1900	1	1
24	♂	immature	110	10	1	1900	1	1
25	♂	immature	110	10	1	1900	1	1
26	♂	immature	110	10	1	1900	1	1
27	♂	immature	110	10	1	1900	1	1
28	♂	immature	110	10	1	1900	1	1
29	♂	immature	110	10	1	1900	1	1
30	♂	immature	110	10	1	1900	1	1
31	♂	immature	110	10	1	1900	1	1
32	♂	immature	110	10	1	1900	1	1
33	♂	immature	110	10	1	1900	1	1
34	♂	immature	110	10	1	1900	1	1
35	♂	immature	110	10	1	1900	1	1
36	♂	immature	110	10	1	1900	1	1
37	♂	immature	110	10	1	1900	1	1
38	♂	immature	110	10	1	1900	1	1
39	♂	immature	110	10	1	1900	1	1
40	♂	immature	110	10	1	1900	1	1
41	♂	immature	110	10	1	1900	1	1
42	♂	immature	110	10	1	1900	1	1
43	♂	immature	110	10	1	1900	1	1
44	♂	immature	110	10	1	1900	1	1
45	♂	immature	110	10	1	1900	1	1
46	♂	immature	110	10	1	1900	1	1
47	♂	immature	110	10	1	1900	1	1
48	♂	immature	110	10	1	1900	1	1
49	♂	immature	110	10	1	1900	1	1
50	♂	immature	110	10	1	1900	1	1
51	♂	immature	110	10	1	1900	1	

[illegible][illegible][illegible]

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                                     -20
ttc att aag acc atg atg atc ctc ttc aat ttg ctc atc ttt ctg tgt      104
Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe Leu Cys
                                     -15      -10      -5
ggc ttc acc aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg      152
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met
                                     1      5      10
cat aaa cct gtt aca atg taaaaaaaa aaaaaa      185
His Lys Pro Val Thr Met
15

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<210> 177
<211> 585
<212> DNA
<213> Homo sapiens

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<220>
<221> sig_peptide
<222> 108..170
<223> Von Heijne matrix
      score 5.5
      seq SFLPSALVIWTS/AF

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<221> polyA_signal
<222> 550..555
<221> polyA_site
<222> 574..585

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<400> 177
cacgttcctg ttgagtacac gttcctgttg atttacaaaa ggtgcaggta tgagcaggtc      60
tgaagactaa cattttgtga agttgtaaaa cagaaaacct gttagaa atg tgg tgg      116
                                     Met Trp Trp
                                     -20
ttt cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca      164
Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr
                                     -15      -10      -5
ttct gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat      212
Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His
                                     1      5      10
ata gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca      260
Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro
15      20      25      30
gaa aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtc tta tgt      308
Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys
35      40      45
caa aaa tagaaatcag gaagataatt caacttaaag aagttcattt catgacccaaa      364
Gln Lys
ctcttcagaa acatgtctttt acaagcatat ctcttgattt gctttctaca ctgttgaatt      424
gtctggcaat atttctgcag tggaaaattt gatttagcta gttcttgact gataaatatg      484
gtaagggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaa      544
tttgaaataa aatgatatga gagtgacaca aaaaaaaaaa a      585

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<210> 178
<211> 613
<212> DNA

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<213> Homo sapiens

<220>
<221> sig_peptide
<222> 118..171
<223> Von Heijne matrix
      score 5.90000009536743
      seq ALALLWSLPASDL/GR

<221> polyA_signal
<222> 583..588

<221> polyA_site
<222> 602..613

<400> 178
ggggtgggtg gactagaagc atttgggagt agtggccagg ggccctggac gctagccacg      60
gagctgccgc acagagcctg gtgtccacaa gcttccaggt tggggttggg gcctggg      117
atg agc ccc ggc agc gcc ttg gcc ctt ctg tgg tcc ctg cca gcc tct      165
Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser
      -15                      -10                      -5
gac ctg ggc cgg tca gtc att gct gga ctc tgg cca cac act ggc gtt      213
Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
      1                      5                      10
ctc atc cac ttg gaa aca agc cag tct ttt ctg caa ggt cag ttg acc      261
Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr
      15                      20                      25                      30
aag agc ata ttt ccc ctc tgt tgt aca tcg ttg ttt tgt gtt tgt gtt      309
Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val
      35                      40                      45
gta aca gtg ggt gga ggg agg gtg ggg tct aca ttt gtt gca      351
Val Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala
      50                      55                      60
tgagtcgatg ggtcagaact ttagtatagc catgcgtcct ctgagtgaca gggcattttg      411
tcgaaaataa gcaccttggg aactaaaccc ctctaatagc tataaaggct ttagttctgt      471
attgattaag ttactgtaaa agcttgggtt tatttttgta ggacttaatg gctaagaatt      531
agaacatagc aagggggctc ctctgttggg gtaatgtaaa ttgtaattat aaataaacat      591
gcaaaccctt aaaaaaaaaa aa                                613

<210> 179
<211> 427
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 128..268
<223> Von Heijne matrix
      score 5.5
      seq SALLFFARPCVFC/FK

<221> polyA_signal
<222> 410..415

<221> polyA_site
<222> 424..427

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<400> 179
agcttggtt tacactgggc aacgtggttg gaatgtatct ggctcagaac tatgatatac      60
caaacctggc taaaaaactt gaagaaatta aaaaggactt ggatgccaag aagaaacccc      120
ctagtgc atg aga ctg cct cca gca ctg cct tca gga tat act gat tct      169
      Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser
            -45                    -40                    -35
act gct ctt gag ggc ctc gtt tac tat ctg aac caa aag ctt ttg ttt      217
Thr Ala Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe
            -30                    -25                    -20
tcg tct cca gcc tca gca ctt ctc ttc ttt gct aga ccc tgt gtt ttt      265
Ser Ser Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe
            -15                    -10                    -5
tgc ttt aaa gca agc aaa atg ggg ccc caa ttt gag aac tac cca aca      313
Cys Phe Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr
      1              5              10              15
ttt cca aca tac tca cct ctt ccc ata atc cct ttc caa ctg cat ggg      361
Phe Pro Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly
            20              25              30
agg ttc taagactgga attatggtgc tagattagta aacatgactt ttaatgaaaa      417
Arg Phe
aaaaacaaaa      427

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<210> 180

<211> 905

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 149..457

<223> Von Heijne matrix

score 4.90000009536743

seq FLLAQTTLRNVLG/TQ

<221> polyA_site

<222> 893..912

<400> 180

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gctgcctggt cttcacactt agctccaaac ccatgaaaaa ttgccaagta taaaagcttc      60
tcaagaatga gatggattct aggggtgtctt cacctgagaa gcaagataaa gagaatttcg      120
tggtgtgtaa caataaacgg cttggtgt atg tgg ctg gat cct gtt ttc cct      172
      Met Trp Leu Asp Pro Val Phe Pro
            -100
ctc ttt cct gtt ggt gat cat tac ctt ccc cat ctc cat atg gat gtg      220
Leu Phe Pro Val Gly Asp His Tyr Leu Pro His Leu His Met Asp Val
      -95              -90              -85              -80
ctt gaa ggt ttg atc ctg gtc ctg cca tgc ata gat gtg ttt gtc aaa      268
Leu Glu Gly Leu Ile Leu Val Leu Pro Cys Ile Asp Val Phe Val Lys
            -75              -70              -65
gtt gac ctc cga aca gtt act tgc aac att cct cca caa gag atc ctc      316
Val Asp Leu Arg Thr Val Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu
            -60              -55              -50
acc aga gac tcc gta act act cag gta gat gga gtt gtc tat tac aga      364
Thr Arg Asp Ser Val Thr Thr Gln Val Asp Gly Val Val Tyr Tyr Arg
            -45              -40              -35
atc tat agt gct gtc tca gca gtg gct aat gtc aac gat gtc cat caa      412
Ile Tyr Ser Ala Val Ser Ala Val Ala Asn Val Asn Asp Val His Gln

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-30          -25          -20
gca aca ttt ctg ctg gct caa acc act ctg aga aat gtc tta ggg aca      460
Ala Thr Phe Leu Leu Ala Gln Thr Thr Leu Arg Asn Val Leu Gly Thr
-15          -10          -5          1
cag acc ttg tcc cag atc tta gct gga cga gaa gag atc gcc cat agc      508
Gln Thr Leu Ser Gln Ile Leu Ala Gly Arg Glu Glu Ile Ala His Ser
5          10          15
atc cag act tta ctt gat gat gcc acc gaa ctg tgg ggg atc cgg gtg      556
Ile Gln Thr Leu Leu Asp Asp Ala Thr Glu Leu Trp Gly Ile Arg Val
20          25          30
gcc cga gtg gaa atc aaa gat gtt cgg att ccc gtg cag ttg cag aga      604
Ala Arg Val Glu Ile Lys Asp Val Arg Ile Pro Val Gln Leu Gln Arg
35          40          45
tcc atg gca gcc gag gct gag gcc acc cgg gaa gcg aga gcc aag gtc      652
Ser Met Ala Ala Glu Ala Glu Ala Thr Arg Glu Ala Arg Ala Lys Val
50          55          60          65
ctt gca gct gaa gga gaa atg aat gct tcc aaa tcc ctg aag tca gcc      700
Leu Ala Ala Glu Gly Glu Met Asn Ala Ser Lys Ser Leu Lys Ser Ala
70          75          80
tcc atg gtg ctg gct gag tct ccc ata gct ctc cag ctg cgc tac ctg      748
Ser Met Val Leu Ala Glu Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu
85          90          95
cag acc ttg agc acg gta gcc acc gag aag aat tct acg att gtg ttt      796
Gln Thr Leu Ser Thr Val Ala Thr Glu Lys Asn Ser Thr Ile Val Phe
100          105          110
cct ctg ccc atg aat ata cta gag ggc att ggt ggc gtc agc tat gat      844
Pro Leu Pro Met Asn Ile Leu Glu Gly Ile Gly Val Ser Tyr Asp
115          120          125
aac cac aag aag ctt cca aat aaa gcc tgagggtcctc ttgcggtagt      891
Asn His Lys Lys Leu Pro Asn Lys Ala
130          135
caaaaaaaaaa aaaa      905

<210> 181
<211> 307
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 181
Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu
-10          -5          1
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
5          10          15
Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
20          25          30          35
Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
40          45          50
Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
55          60          65
Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys
70          75          80
Lys Thr Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg
85          90          95

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Ala	Gly	Pro	Asn	Gly	Thr	Leu	Phe	Val	Ala	Asp	Ala	Tyr	Lys	Gly	Leu
100					105					110					115
Phe	Glu	Val	Asn	Pro	Trp	Lys	Arg	Glu	Val	Lys	Leu	Leu	Leu	Ser	Ser
			120						125						130
Glu	Thr	Pro	Ile	Glu	Gly	Lys	Asn	Met	Ser	Phe	Val	Asn	Asp	Leu	Thr
			135					140							145
Val	Thr	Gln	Asp	Gly	Arg	Lys	Ile	Tyr	Phe	Thr	Asp	Ser	Ser	Ser	Lys
		150					155								160
Trp	Gln	Arg	Arg	Asp	Tyr	Leu	Leu	Val	Met	Glu	Gly	Thr	Asp	Asp	
		165				170									
Gly	Arg	Leu	Leu	Glu	Tyr	Asp	Thr	Val	Thr	Arg	Glu	Val	Lys	Val	Leu
180					185					190					195
Leu	Asp	Gln	Leu	Arg	Phe	Pro	Asn	Gly	Val	Gln	Leu	Ser	Pro	Ala	Glu
			200						205						210
Asp	Phe	Val	Leu	Val	Ala	Glu	Thr	Thr	Met	Ala	Arg	Ile	Arg	Arg	Val
			215					220							225
Tyr	Val	Ser	Gly	Leu	Met	Lys	Gly	Gly	Ala	Asp	Leu	Phe	Val	Glu	Asn
		230					235								240
Met	Pro	Gly	Phe	Pro	Asp	Asn	Ile	Arg	Pro	Ser	Ser	Ser	Gly	Gly	Tyr
		245				250									255
Trp	Val	Gly	Met	Ser	Thr	Ile	Arg	Pro	Asn	Pro	Gly	Phe	Ser	Met	Leu
260					265					270					275
Asp	Phe	Leu	Ser	Glu	Arg	Pro	Trp	Ile	Lys	Arg	Met	Ile	Phe	Lys	Val
				280					285						290
Lys	Lys	Lys													

<210> 182
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>

<400> 182

Met	Met	Tyr	Val	Ser	Ile	Glu	Met	Ser	Gly	Pro	Thr	Ile	Ser	His	Leu
1				5					10					15	
Phe	Asp	Tyr	Val	Val	Cys	Tyr	Ile	Tyr	Gly	Leu	Lys	Ser	Phe	Ser	Leu
			20					25					30		
Lys	Gln	Leu	Lys	Lys	Lys	Ser	Trp	Ser	Lys	Tyr	Leu	Phe	Glu	Ser	Cys
		35					40					45			
Cys	Tyr	Arg	Ser	Leu	Tyr	Val	Cys	Val	Phe	Ile					
	50					55									

<210> 183
 <211> 97
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -28..-1

<400> 183

Met	Ser	Pro	Ala	Phe	Arg	Ala	Met	Asp	Val	Glu	Pro	Arg	Ala	Lys	Gly
			-25					-20					-15		
Val	Leu	Leu	Glu	Pro	Phe	Val	His	Gln	Val	Gly	Gly	His	Ser	Cys	Val

-10 -5 1
 Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu
 5 10 15 20
 His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Ser Pro
 25 30 35
 Gln Tyr Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp Pro Ser Leu
 40 45 50
 Pro His Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln Gly Ser Val
 55 60 65
 Ala

<210> 184
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 184

Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala
 -30 -25 -20
 Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro
 -15 -10 -5
 Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser
 1 5 10 15
 Thr Phe Ala His
 20

<210> 185
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -97..-1

<400> 185

Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val
 -95 -90 -85
 Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val
 -80 -75 -70
 Val Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly
 -65 -60 -55 -50
 Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly
 -45 -40 -35
 Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val
 -30 -25 -20
 Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser
 -15 -10 -5
 Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro
 1 5 10 15
 Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser
 20 25

<210> 186
 <211> 230
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 186
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
 -20 -15 -10
 Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
 -5 1 5
 Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
 10 15 20
 Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys
 25 30 35 40
 Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala
 45 50 55
 Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile
 60 65 70
 Ile Ser Val Val Gly Met Arg Cys Thr Val Phe Cys Gln Glu Ser Arg
 75 80 85
 Ala Lys Asp Arg Val Ala Val Ala Gly Gly Val Phe Phe Ile Leu Gly
 90 95 100
 Gly Leu Leu Gly Phe Ile Pro Val Ala Trp Asn Leu His Gly Ile Leu
 105 110 115 120
 Arg Asp Phe Tyr Ser Pro Leu Val Pro Asp Ser Met Lys Phe Glu Ile
 125 130 135
 Gly Glu Ala Leu Tyr Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile
 140 145 150
 Ala Gly Ile Ile Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser
 155 160 165
 Asn Tyr Tyr Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser
 170 175 180
 Pro Arg Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr
 185 190 195 200
 Ser Leu Thr Gly Tyr Val
 205

<210> 187
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 187
 Met Phe Ala Leu Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Ala Gly Gly Ser Phe Gly
 -15 -10 -5

Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
 1 5 10 15
 Asp Pro Glu Leu Glu Lys Lys Pro Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
 Ser Glu Tyr Glu Gly Ser Ile Cys
 35 40

<210> 188
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33..-1

<400> 188
 Met Ser Gln Thr Ala Trp Leu Ser Leu Leu Ser Ser Ser Pro Phe Gly
 -30 -25 -20
 Pro Phe Ser Ala Leu Thr Phe Leu Phe Leu His Leu Pro Pro Ser Thr
 -15 -10 -5
 Ser Leu Phe Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly Pro Leu Gly
 1 5 10 15
 Leu Ile Leu Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys Cys Asp Phe
 20 25 30
 Ala Leu Ser Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe Ser Ile Met
 35 40 45
 Asp Pro Lys Arg Lys Thr Lys Cys
 50 55

<210> 189
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 189
 Met Phe Ala Pro Ala Val Thr Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
 -15 -10 -5
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
 1 5 10 15
 Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
 Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
 35 40 45
 Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
 50 55 60
 Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
 65 70

<210> 190
 <211> 267
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 190

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Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
-20 -15 -10
Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
-5 1 5 10
Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
15 20 25
Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
30 35 40
Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala
45 50 55
Leu Ser Pro Glu Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu
60 65 70 75
Val Leu Gly Ile Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe
80 85 90
Gln Lys Thr Thr Leu Phe Ala Ala His Val Ser Gly Ala Val Leu Thr
95 100 105
Phe Gly Met Gly Ser Leu Tyr Met Phe Val Gln Thr Ile Leu Ser Tyr
110 115 120
Gln Met Gln Pro Lys Ile His Gly Lys Gln Val Phe Trp Ile Arg Leu
125 130 135
Leu Leu Val Ile Trp Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys
140 145 150 155
Ser Ser Val Leu His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys
160 165 170
Leu His Trp Asn Pro Glu Asp Lys Gly Tyr Ala Leu His Met Ile Thr
175 180 185
Thr Ala Ala Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu
190 195 200
Thr Tyr Ile Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn
205 210 215
Leu His Gly Leu Thr Leu Tyr Asp Thr Ala Pro Cys Pro Ile Asn Asn
220 225 230 235
Glu Arg Thr Arg Leu Leu Ser Arg Asp Ile Arg
240 245

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<210> 191
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>

<400> 191

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Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile
1 5 10 15
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
20 25 30

```

Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 35 40 45
 Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
 50 55 60
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 65 70 75 80
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 85 90 95
 Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr
 100 105

<210> 192
 <211> 69
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -46..-1

<400> 192
 Met Ser Val Phe Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile
 -45 -40 -35
 Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys
 -30 -25 -20 -15
 Ser Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu
 -10 -5 1
 Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Leu
 5 10 15
 Lys Tyr His Trp Pro
 20

<210> 193
 <211> 251
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 193
 Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro
 -25 -20 -15
 Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr
 -10 -5 1
 Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro
 5 10 15 20
 Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys Val Arg Arg
 25 30 35
 Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr
 40 45 50
 Glu Phe Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly Gly Gly Tyr
 55 60 65
 Leu His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile Asn Arg Ser
 70 75 80

Met	Asp	Pro	Lys	Asn	Met	Phe	Ala	Ile	Trp	Arg	Val	Pro	Ala	Pro	Phe
85					90					95					100
Lys	Pro	Ile	Thr	Arg	Lys	Ser	Val	Gly	His	Arg	Met	Gly	Gly	Gly	Lys
				105					110						115
Gly	Ala	Ile	Asp	His	Tyr	Val	Thr	Pro	Val	Lys	Ala	Gly	Arg	Leu	Val
			120					125					130		
Val	Glu	Met	Gly	Gly	Arg	Cys	Glu	Phe	Glu	Glu	Val	Gln	Gly	Phe	Leu
		135					140					145			
Asp	Gln	Val	Ala	His	Lys	Leu	Pro	Phe	Ala	Ala	Lys	Ala	Val	Ser	Arg
		150				155						160			
Gly	Thr	Leu	Glu	Lys	Met	Arg	Lys	Asp	Gln	Glu	Glu	Arg	Glu	Arg	Asn
165					170				175						180
Asn	Gln	Asn	Pro	Trp	Thr	Phe	Glu	Arg	Ile	Ala	Thr	Ala	Asn	Met	Leu
				185					190						195
Gly	Ile	Arg	Lys	Val	Leu	Ser	Pro	Tyr	Asp	Leu	Thr	His	Lys	Gly	Lys
			200					205						210	
Tyr	Trp	Gly	Lys	Phe	Tyr	Met	Pro	Lys	Arg	Val					
		215					220								

<210> 194
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -48..-1

<400> 194

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe	Ser
			-45					-40					-35		
Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Asp	Ile	Ile	Asn	Ser	Leu
		-30					-25					-20			
Val	Thr	Thr	Val	Phe	Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro
		-15				-10					-5				
Glu	Thr	Thr	Thr	Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr
1				5				10						15	
Ala	Val	Cys	Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu
			20					25					30		
Phe	Asn	Pro	Ser	Gly	Pro	Tyr	Gln	Lys	Lys	Pro	Val	His	Glu	Lys	Lys
		35					40					45			
Glu	Val	Leu													
		50													

<210> 195
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 195

Met	Ser	Asn	Thr	His	Thr	Val	Leu	Val	Ser	Leu	Pro	His	Pro	His	Pro
		-30				-25					-20				

Ala Leu Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro
 -15 -10 -5 1
 Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser
 5 10 15
 Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser
 20 25 30
 Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp
 35 40 45
 Leu
 50

<210> 196
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>

<400> 196

Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu Leu Thr
 1 5 10 15
 Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp His Gly
 20 25 30
 Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu Glu Pro
 35 40 45
 Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys Tyr Tyr Ile
 50 55 60
 Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser Phe Phe
 65 70 75 80
 Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu Arg Lys Val
 85 90 95
 Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val Ser His Leu
 100 105 110
 Gly Ile Leu Ala Val Gln Glu Gly Lys His Phe His Ser His Asn His
 115 120 125
 Gln His Ser His Asn His Leu Asn Ser Glu Asn Gln Thr Val Thr Ser
 130 135 140
 Val Ser Thr Lys Lys Lys
 145 150

<210> 197
 <211> 273
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
 <222> -45..-1

<400> 197

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
 -45 -40 -35 -30
 Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
 -25 -20 -15
 Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
 -10 -5 1

Lys	Asp	Phe	Asp	Cys	Asn	Thr	Arg	Gln	Pro	Gly	Cys	Ser	Asn	Val	Cys	
5						10					15					
Phe	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln	
20					25					30					35	
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala	
				40					45						50	
Tyr	Arg	Glu	Val	Gln	Glu	Lys	Arg	His	Arg	Glu	Ala	His	Gly	Glu	Asn	
			55					60					65			
Ser	Gly	Arg	Leu	Tyr	Leu	Asn	Pro	Gly	Lys	Lys	Arg	Gly	Gly	Leu	Trp	
		70				75						80				
Trp	Thr	Tyr	Val	Cys	Ser	Leu	Val	Phe	Lys	Ala	Ser	Val	Asp	Ile	Ala	
		85				90					95					
Phe	Leu	Tyr	Val	Phe	His	Ser	Phe	Tyr	Pro	Lys	Tyr	Ile	Leu	Pro	Pro	
100					105					110					115	
Val	Val	Lys	Cys	His	Ala	Asp	Pro	Cys	Pro	Asn	Ile	Val	Asp	Cys	Phe	
				120					125					130		
Ile	Ser	Lys	Pro	Ser	Glu	Lys	Asn	Ile	Phe	Thr	Leu	Phe	Met	Val	Ala	
			135					140					145			
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu	Ile	Tyr	Leu	
		150					155					160				
Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys	Ala	Gln	Ala	
		165				170					175					
Met	Cys	Thr	Gly	His	His	Pro	His	Asp	Thr	Thr	Ser	Ser	Cys	Lys	Gln	
180					185					190					195	
Asp	Asp	Leu	Leu	Ser	Gly	Asp	Leu	Ile	Phe	Leu	Gly	Ser	Asp	Ser	His	
				200					205					210		
Pro	Pro	Leu	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys	Lys	Thr	Ile	
			215					220					225			
Leu																

<210> 198
 <211> 413
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -37..-1

<400> 198																
Met	Ala	Ser	Lys	Ile	Leu	Leu	Asn	Val	Gln	Glu	Glu	Val	Thr	Cys	Pro	
		-35					-30					-25				
Ile	Cys	Leu	Glu	Leu	Leu	Thr	Glu	Pro	Leu	Ser	Leu	Asp	Cys	Gly	His	
	-20					-15					-10					
Ser	Leu	Cys	Arg	Ala	Cys	Ile	Thr	Val	Ser	Asn	Lys	Glu	Ala	Val	Thr	
-5					1				5					10		
Ser	Met	Gly	Gly	Lys	Ser	Ser	Cys	Pro	Val	Cys	Gly	Ile	Ser	Tyr	Ser	
		15					20					25				
Phe	Glu	His	Leu	Gln	Ala	Asn	Gln	His	Leu	Ala	Asn	Ile	Val	Glu	Arg	
	30					35					40					
Leu	Lys	Glu	Val	Lys	Leu	Ser	Pro	Asp	Asn	Gly	Lys	Lys	Arg	Asp	Leu	
	45					50				55						
Cys	Asp	His	His	Gly	Glu	Lys	Leu	Leu	Leu	Phe	Cys	Lys	Glu	Asp	Arg	
60					65					70					75	
Lys	Val	Ile	Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	Glu	His	Arg	Gly	His	
			80						85					90		
His	Thr	Val	Leu	Thr	Glu	Glu	Val	Phe	Lys	Glu	Cys	Gln	Glu	Lys	Leu	

	95		100		105										
Gln	Ala	Val	Leu	Lys	Arg	Leu	Lys	Lys	Glu	Glu	Glu	Glu	Ala	Glu	Lys
	110						115					120			
Leu	Glu	Ala	Asp	Ile	Arg	Glu	Glu	Lys	Thr	Ser	Trp	Lys	Tyr	Gln	Val
	125						130					135			
Gln	Thr	Glu	Arg	Gln	Arg	Ile	Gln	Thr	Glu	Phe	Asp	Gln	Leu	Arg	Ser
	140						145				150				155
Ile	Leu	Asn	Asn	Glu	Glu	Gln	Arg	Glu	Leu	Gln	Arg	Leu	Glu	Glu	Glu
			160						165					170	
Glu	Lys	Lys	Thr	Leu	Asp	Lys	Phe	Ala	Glu	Ala	Glu	Asp	Glu	Leu	Val
			175					180						185	
Gln	Gln	Lys	Gln	Leu	Val	Arg	Glu	Leu	Ile	Ser	Asp	Val	Glu	Cys	Arg
	190						195					200			
Ser	Gln	Trp	Ser	Thr	Met	Glu	Leu	Leu	Gln	Asp	Met	Ser	Gly	Ile	Met
	205					210				215					
Lys	Trp	Ser	Glu	Ile	Trp	Arg	Leu	Lys	Lys	Pro	Lys	Met	Val	Ser	Lys
	220				225					230					235
Lys	Leu	Lys	Thr	Val	Phe	His	Ala	Pro	Asp	Leu	Ser	Arg	Met	Leu	Gln
			240						245					250	
Met	Phe	Arg	Glu	Leu	Thr	Ala	Val	Arg	Cys	Tyr	Trp	Val	Asp	Val	Thr
			255					260					265		
Leu	Asn	Ser	Val	Asn	Leu	Asn	Leu	Asn	Leu	Val	Leu	Ser	Glu	Asp	Gln
	270					275						280			
Arg	Gln	Val	Ile	Ser	Val	Pro	Ile	Trp	Pro	Phe	Gln	Cys	Tyr	Asn	Tyr
	285					290					295				
Gly	Val	Leu	Gly	Ser	Gln	Tyr	Phe	Ser	Ser	Gly	Lys	His	Tyr	Trp	Glu
	300				305					310					315
Val	Asp	Val	Ser	Lys	Lys	Thr	Ala	Trp	Ile	Leu	Gly	Val	Tyr	Cys	Arg
			320						325					330	
Thr	Tyr	Ser	Arg	His	Met	Lys	Tyr	Val	Val	Arg	Arg	Cys	Ala	Asn	Arg
		335						340					345		
Gln	Asn	Leu	Tyr	Thr	Lys	Tyr	Arg	Pro	Leu	Phe	Gly	Tyr	Trp	Val	Ile
	350					355						360			
Gly	Leu	Gln	Asn	Lys	Cys	Lys	Tyr	Gly	Ala	Lys	Lys	Lys			
	365					370					375				

<210> 199
 <211> 393
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> SIGNAL
 <222> -19..-1

<400> 199
 Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
 -15 -10 -5
 Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys
 1 5 10
 Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg
 15 20 25
 Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His
 30 35 40 45
 Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp
 50 55 60
 Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr

-10					-5					1				5	
Met	Cys	Leu	Lys	Ile	Ile	Arg	Glu	Tyr	Glu	Arg	Ala	Val	Val	Phe	Arg
			10					15					20		
Leu	Gly	Arg	Ile	Gln	Ala	Asp	Lys	Ala	Lys	Gly	Pro	Gly	Leu	Ile	Leu
		25					30					35			
Val	Leu	Pro	Cys	Ile	Asp	Val	Phe	Val	Lys	Val	Asp	Leu	Arg	Thr	Val
	40				45					50					
Thr	Cys	Asn	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Arg	Asp	Ser	Val	Thr
55				60						65				70	
Thr	Gln	Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Ile	Tyr	Ser	Ala	Val	Ser
			75					80					85		
Ala	Val	Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe	Leu	Leu	Ala
			90					95					100		
Gln	Thr	Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Gln	Thr	Leu	Ser	Gln	Ile
	105						110					115			
Leu	Ala	Gly	Arg	Glu	Glu	Ile	Ala	His	Ser	Ile	Gln	Thr	Leu	Leu	Asp
	120				125					130					
Asp	Ala	Thr	Glu	Leu	Trp	Gly	Ile	Arg	Val	Ala	Arg	Val	Glu	Ile	Lys
135				140					145					150	
Asp	Val	Arg	Ile	Pro	Val	Gln	Leu	Gln	Arg	Ser	Met	Ala	Ala	Glu	Ala
			155					160					165		
Glu	Ala	Thr	Arg	Glu	Ala	Arg	Ala	Lys	Val	Leu	Ala	Ala	Glu	Gly	Glu
			170					175					180		
Met	Ser	Ala	Ser	Lys	Ser	Leu	Lys	Ser	Ala	Ser	Met	Val	Leu	Ala	Glu
	185						190					195			
Ser	Pro	Ile	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	Gln	Thr	Leu	Ser	Thr	Val
	200					205					210				
Ala	Thr	Glu	Lys	Asn	Ser	Thr	Ile	Val	Phe	Pro	Leu	Pro	Met	Asn	Ile
215				220					225					230	
Leu	Glu	Gly	Ile	Gly	Gly	Val	Ser	Tyr	Asp	Asn	His	Lys	Lys	Leu	Pro
			235					240						245	
Asn	Lys	Ala													

<210> 202
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>

<400> 202

Met	Pro	Pro	Arg	Asn	Leu	Leu	Glu	Leu	Leu	Ile	Asn	Ile	Lys	Ala	Gly
1				5					10				15		
Thr	Tyr	Leu	Pro	Gln	Ser	Tyr	Leu	Ile	His	Glu	His	Met	Val	Ile	Thr
		20					25					30			
Asp	Arg	Ile	Glu	Asn	Ile	Asp	His	Leu	Gly	Phe	Phe	Ile	Tyr	Arg	Leu
	35					40					45				
Cys	His	Asp	Lys	Glu	Thr	Tyr	Lys	Leu	Gln	Arg	Arg	Glu	Thr	Ile	Lys
	50				55					60					
Gly	Ile	Gln	Lys	Arg	Glu	Ala	Ser	Asn	Cys	Phe	Ala	Ile	Arg	His	Phe
65				70					75					80	
Glu	Asn	Lys	Phe	Ala	Val	Glu	Thr	Leu	Ile	Cys	Ser				
			85					90							

<210> 203
 <211> 127

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -63..-1

<400> 203

```
Met Ser Ala Ala Gly Ala Arg Gly Leu Arg Ala Thr Tyr His Arg Leu
      -60      -55      -50
Pro Asp Lys Val Glu Leu Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr
      -45      -40      -35
Asn His Pro Ala Gly Pro Arg Thr Val Phe Phe Trp Ala Pro Ile Met
      -30      -25      -20
Lys Trp Gly Leu Val Cys Ala Gly Leu Ala Asp Met Ala Arg Pro Ala
      -15      -10      -5      1
Glu Lys Leu Ser Thr Ala Gln Ser Ala Val Leu Met Ala Thr Gly Phe
      5      10      15
Ile Trp Ser Arg Tyr Ser Leu Val Ile Ile Pro Lys Asn Trp Ser Leu
      20      25      30
Phe Ala Val Asn Phe Phe Val Gly Ala Ala Gly Ala Ser Gln Leu Phe
      35      40      45
Arg Ile Trp Arg Tyr Asn Gln Glu Leu Lys Ala Lys Ala His Lys
50      55      60
```

<210> 204
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 204

```
Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
-20      -15      -10      -5
Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
      1      5      10
Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
      15      20      25
Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln
      30      35      40
Ser Val Val Glu Val Thr Val Thr Val Pro Pro Asn Lys Val Ala His
45      50      55      60
Ser Gly Phe Gly
```

<210> 205
<211> 182
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 205

Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
-20 -15 -10 -5
Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
1 5 10
Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
15 20 25
Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln
30 35 40
Ser Val Val Glu Val Pro Tyr Ala Arg Ser Glu Ala His Leu Thr Glu
45 50 55 60
Leu Leu Glu Glu Ile Cys Asp Arg Met Lys Glu Tyr Gly Glu Gln Ile
65 70 75
Asp Pro Ser Thr His Arg Lys Asn Tyr Val Arg Val Val Gly Arg Asn
80 85 90
Gly Glu Ser Ser Glu Leu Asp Leu Gln Gly Ile Arg Ile Asp Ser Asp
95 100 105
Ile Ser Gly Thr Leu Lys Phe Ala Cys Gly Ser Ile Val Glu Glu Tyr
110 115 120
Glu Asp Glu Leu Ile Glu Phe Phe Ser Arg Glu Ala Asp Asn Val Lys
125 130 135 140
Asp Lys Leu Cys Ser Lys Arg Thr Asp Leu Cys Asp His Ala Leu His
145 150 155
Ile Ser His Asp Glu Leu
160

<210> 206

<211> 71

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25..-1

<400> 206

Met Pro Ala Gly Val Pro Met Ser Thr Tyr Leu Lys Met Phe Ala Ala
-25 -20 -15 -10
Ser Leu Leu Ala Met Cys Ala Gly Ala Glu Val Val His Arg Tyr Tyr
-5 1 5
Arg Pro Asp Leu Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu
10 15 20
Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro Gln Val
25 30 35
Ser Gln Gln Glu Glu Leu Lys
40 45

<210> 207

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<400> 207

Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe Leu

<400> 205

```
Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
-20          -15          -10          -5
Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
      1          5          10
Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
      15          20          25
Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln
      30          35          40
Ser Val Val Glu Val Pro Tyr Ala Arg Ser Glu Ala His Leu Thr Glu
      45          50          55          60
Leu Leu Glu Glu Ile Cys Asp Arg Met Lys Glu Tyr Gly Glu Gln Ile
      65          70          75
Asp Pro Ser Thr His Arg Lys Asn Tyr Val Arg Val Val Gly Arg Asn
      80          85          90
Gly Glu Ser Ser Glu Leu Asp Leu Gln Gly Ile Arg Ile Asp Ser Asp
      95          100          105
Ile Ser Gly Thr Leu Lys Phe Ala Cys Gly Ser Ile Val Glu Glu Tyr
      110          115          120
Glu Asp Glu Leu Ile Glu Phe Phe Ser Arg Glu Ala Asp Asn Val Lys
      125          130          135          140
Asp Lys Leu Cys Ser Lys Arg Thr Asp Leu Cys Asp His Ala Leu His
      145          150          155
Ile Ser His Asp Glu Leu
      160
```

<210> 206

<211> 71

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25..-1

<400> 206

```
Met Pro Ala Gly Val Pro Met Ser Thr Tyr Leu Lys Met Phe Ala Ala
-25          -20          -15          -10
Ser Leu Leu Ala Met Cys Ala Gly Ala Glu Val Val His Arg Tyr Tyr
      -5          1          5
Arg Pro Asp Leu Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu
      10          15          20
Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro Gln Val
      25          30          35
Ser Gln Gln Glu Glu Leu Lys
      40          45
```

<210> 207

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<400> 207

Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe Leu

1		5		10		15									
Cys	Thr	Asp	Arg	Asp	Cys	Asn	Val	Ile	Leu	Gly	Ser	Ala	Gln	Glu	Phe
		20						25					30		
Leu	Lys	Pro	Ser	Asp	Ser	Phe	Ser	Ala	Gly	Glu	Pro	Arg	Val	Leu	Gly
		35					40					45			
Leu	Ala	Met	Val	Pro	Gly	His	His	Ile	Val	Ser	Ile	Glu	Val	Gln	Arg
	50					55					60				
Glu	Ser	Leu	Thr	Gly	Pro	Pro	Tyr	Leu							
65					70										

<210> 208
 <211> 169
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -150..-1

<400> 208

Met	Ala	Glu	Thr	Lys	Asp	Thr	Ala	Gln	Met	Leu	Val	Thr	Phe	Lys	Asp
-150					-145				-140						-135
Val	Ala	Val	Thr	Phe	Thr	Arg	Glu	Glu	Trp	Arg	Gln	Leu	Asp	Leu	Ala
				-130					-125						-120
Gln	Arg	Thr	Leu	Tyr	Arg	Glu	Gly	Ile	Gly	Phe	Pro	Lys	Pro	Glu	Leu
			-115					-110					-105		
Val	His	Leu	Leu	Glu	His	Gly	Gln	Glu	Leu	Trp	Ile	Val	Lys	Arg	Gly
		-100				-95					-90				
Leu	Ser	His	Ala	Thr	Cys	Ala	Glu	Phe	His	Ser	Cys	Cys	Pro	Gly	Trp
-85					-80					-75					
Ser	Ala	Val	Xaa	Arg	His	Leu	Ser	Ser	Leu	Gln	Leu	Leu	Pro	Pro	Glu
-70				-65					-60						-55
Phe	Lys	Gly	Phe	Ser	Cys	Leu	Ser	Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Arg
			-50					-45					-40		
Arg	Pro	Pro	Pro	Cys	Pro	Ala	Gly	Phe	Phe	Val	Phe	Leu	Val	Glu	Thr
		-35					-30					-25			
Gly	Leu	His	Val	Gly	Gln	Ala	Gly	Leu	Glu	Leu	Leu	Thr	Ser	Cys	
	-20				-15				-10						
Ser	Pro	Pro	Ala	Ser	Ala	Ser	Gln	Ser	Ala	Ala	Ile	Thr	Gly	Val	Ser
-5				1				5						10	
His	Arg	Ala	Arg	Gln	Arg	Lys	Thr	Ala							
			15												

<210> 209
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 209

Met	Glu	Leu	Ile	Ser	Pro	Thr	Val	Ile	Ile	Ile	Leu	Gly	Cys	Leu	Ala
	-20						-15				-10				
Leu	Phe	Leu	Leu	Leu	Gln	Arg	Lys	Asn	Leu	Arg	Arg	Pro	Pro	Cys	Ile

-5		1		5		10
Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala						
	15		20		25	
Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Val Cys Gly Arg Gly						
	30		35		40	
Arg Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu Phe						
	45		50			

<210> 210
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54..-1

<400> 210
Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys Asp
Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala
Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu Leu
Val Ser Leu Val Glu Ser Ile Trp Leu His Ile Thr Glu Asn Gln Ile
Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu Lys
Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln

<210> 211
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 211
Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala
Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Tyr Gly Pro Ile Phe
Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe Val Thr Glu Glu Glu
Gly Ile Asn Val Phe Leu Lys Ser Lys Lys Lys Lys

<210> 212

<211> 89
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 212
 Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
 -15 -10 -5
 Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
 1 5 10 15
 Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
 20 25 30
 Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile
 35 40 45
 Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala
 50 55 60
 Glu Ala Gly Ala Ser Leu Tyr Ser Pro
 65 70

<210> 213
 <211> 109
 <212> PRT
 <213> Homo sapiens

<220>

<400> 213
 Met Lys Val Asp Lys Asp Arg Gln Met Val Val Leu Glu Glu Glu Phe
 1 5 10 15
 Arg Asn Ile Ser Pro Glu Glu Leu Lys Met Glu Leu Pro Glu Arg Gln
 20 25 30
 Pro Arg Phe Val Val Tyr Ser Tyr Lys Tyr Val Arg Asp Asp Gly Arg
 35 40 45
 Val Ser Tyr Pro Leu Cys Phe Ile Phe Ser Ser Pro Val Gly Cys Lys
 50 55 60
 Pro Glu Gln Gln Met Met Tyr Ala Gly Ser Lys Asn Arg Leu Val Gln
 65 70 75 80
 Thr Ala Glu Leu Thr Lys Val Phe Glu Ile Arg Thr Thr Asp Asp Leu
 85 90 95
 Thr Glu Ala Trp Leu Gln Glu Lys Leu Ser Phe Phe Arg
 100 105

<210> 214
 <211> 114
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -103..-1

<400> 214
 Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile

-5						1				5					10
Leu	Glu	Pro	Pro	Pro	Cys	Ile	Ser	Ala	Pro	Glu	Asn	Cys	Thr	His	Leu
				15					20					25	
Cys	Thr	Met	Gln	Glu	Asp	Cys	Glu	Lys	Gly	Phe	Gln	Cys	Cys	Ser	Ser
			30					35					40		
Phe	Cys	Gly	Ile	Val	Cys	Ser	Ser	Glu	Thr	Phe	Gln	Lys	Arg	Asn	Arg
		45					50					55			
Ile	Lys	His	Lys	Gly	Ser	Glu	Val	Ile	Met	Pro	Ala	Asn			
	60					65					70				

<210> 217
 <211> 207
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

<400> 217

Met	His	Ile	Leu	Gln	Leu	Leu	Thr	Thr	Val	Asp	Asp	Gly	Ile	Gln	Ala
		-40					-35					-30			
Ile	Val	His	Cys	Pro	Asp	Thr	Gly	Lys	Asp	Ile	Trp	Asn	Leu	Leu	Phe
	-25					-20					-15				
Asp	Leu	Val	Cys	His	Glu	Phe	Cys	Gln	Ser	Asp	Asp	Pro	Pro	Ile	Ile
	-10				-5					1				5	
Leu	Gln	Glu	Gln	Lys	Thr	Val	Leu	Ala	Ser	Val	Phe	Ser	Val	Leu	Ser
		10						15					20		
Ala	Ile	Tyr	Ala	Ser	Gln	Thr	Glu	Gln	Glu	Tyr	Leu	Lys	Ile	Glu	Lys
	25						30					35			
Val	Asp	Leu	Pro	Leu	Ile	Asp	Ser	Leu	Ile	Arg	Val	Leu	Gln	Asn	Met
	40					45					50				
Glu	Gln	Cys	Gln	Lys	Lys	Pro	Glu	Asn	Ser	Ala	Glu	Ser	Asn	Thr	Glu
	55				60					65					70
Glu	Thr	Lys	Arg	Thr	Asp	Leu	Thr	Gln	Asp	Asp	Phe	His	Leu	Lys	Ile
			75					80						85	
Leu	Lys	Asp	Ile	Leu	Cys	Glu	Phe	Leu	Ser	Asn	Ile	Phe	Gln	Ala	Leu
		90						95					100		
Thr	Lys	Glu	Thr	Val	Ala	Gln	Gly	Val	Lys	Glu	Gly	Gln	Leu	Ser	Lys
	105						110					115			
Gln	Lys	Cys	Ser	Ser	Ala	Phe	Gln	Asn	Leu	Leu	Pro	Phe	Tyr	Ser	Pro
	120					125					130				
Val	Val	Glu	Asp	Phe	Ile	Lys	Ile	Leu	Arg	Glu	Val	Asp	Lys	Ala	Leu
	135				140					145					150
Ala	Asp	Asp	Leu	Glu	Lys	Asn	Phe	Pro	Ser	Leu	Lys	Val	Gln	Thr	
			155						160					165	

<210> 218
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>

<400> 218

Met Pro His Ser Lys Pro Leu Asp Trp Gly Leu Ser Ser Val Ala Glu

1		5		10		15									
Cys	Pro	Ala	Glu	Leu	Phe	Pro	Ser	Thr	Gly	Gly	Leu	Ala	Gly	Lys	Gly
		20					25						30		
Pro	Gly	Leu	Asp	Ile	Leu	Arg	Cys	Val	Leu	Ser	Pro	Trp	Ala	Ser	His
		35					40					45			
Phe	Pro	Ser	Leu	Ser	Leu	Gly	Val	Phe	Asn	Leu					
	50					55									

<210> 219
 <211> 56
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 219
Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu
-25 -20 -15
Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg
-10 -5 1 5
Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val Arg Ala
10 15 20
Trp Cys Ile Gln Pro Trp Ala Lys
25

<210> 220
 <211> 162
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -94..-1

<400> 220
Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
-90 -85 -80
Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
-75 -70 -65
Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala
-60 -55 -50
Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe
-45 -40 -35
Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly
-30 -25 -20 -15
Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His
-10 -5 1
Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp
5 10 15
Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val
20 25 30
Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro
35 40 45 50
His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val

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60

65

Arg Arg

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<212> PRT

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<222> -68..-1

<400> 221

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Pro	Pro	Pro	Ser	Lys	Gln	Ser	Leu	Phe	Cys	Pro	Lys	Ser	Lys
		-50				-45					-40		Leu
His	Ile	His	Arg	Ala	Glu	Ile	Ser	Lys	Ile	Met	Arg	Glu	Cys
	-35					-30				-25			Gln
Glu	Ser	Phe	Trp	Lys	Arg	Ala	Leu	Pro	Phe	Ser	Leu	Val	Ser
	-20				-15				-10				Met
Val	Thr	Gln	Gly	Leu	Val	Tyr	Gln	Gly	Tyr	Leu	Ala	Ala	Asn
				1				5				10	Ser
Phe	Gly	Ser	Leu	Pro	Lys	Val	Ala	Leu	Ala	Gly	Leu	Leu	Gly
		15					20				25		Phe
Leu	Gly	Lys	Val	Ser	Tyr	Ile	Gly	Val	Cys	Gln	Ser	Lys	Phe
	30					35				40			His
Phe	Glu	Asp	Gln	Leu	Arg	Gly	Ala	Gly	Phe	Gly	Pro	Gln	His
	45				50					55			Asn
His	Cys	Leu	Leu	Thr	Cys	Glu	Glu	Cys	Lys	Ile	Lys	His	Gly
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Glu	Lys	Gly	Asp	Ser	Gln	Pro	Ser	Ala	Ser				Ser
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<210> 222

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<400> 222

Met	Lys	Val	Glu	Glu	Glu	His	Thr	Asn	Ala	Ile	Gly	Thr	Leu	His	Gly
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Gly	Leu	Thr	Ala	Thr	Leu	Val	Asp	Asn	Ile	Ser	Thr	Met	Ala	Leu	Leu
			20					25					30		
Cys	Thr	Glu	Arg	Gly	Ala	Pro	Gly	Val	Ser	Val	Asp	Met	Asn	Ile	Thr
		35					40					45			
Tyr	Met	Ser	Pro	Ala	Lys	Leu	Gly	Glu	Asp	Ile	Val	Ile	Thr	Ala	His
	50					55					60				
Val	Leu	Lys	Gln	Gly	Lys	Thr	Leu	Ala	Phe	Thr	Ser	Val	Gly	Leu	Thr
	65				70					75				80	
Asn	Lys	Ala	Thr	Gly	Lys	Leu	Ile	Ala	Gln	Gly	Arg	His	Thr	Lys	His
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Leu	Gly	Asn													

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<400> 223
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 Pro Tyr Phe Lys Met His Lys Pro Val Thr Met
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 -5 1 5 10
 Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
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 Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
 30 35 40
 Val Leu Cys Gln Lys
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<210> 225
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 1 5 10
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 15 20 25 30
 Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val

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<400> 226

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	-30					-25					-20				
Pro	Ala	Ser	Ala	Leu	Leu	Phe	Phe	Ala	Arg	Pro	Cys	Val	Phe	Cys	Phe
-15				-10					-5						1
Lys	Ala	Ser	Lys	Met	Gly	Pro	Gln	Phe	Glu	Asn	Tyr	Pro	Thr	Phe	Pro
		5						10					15		
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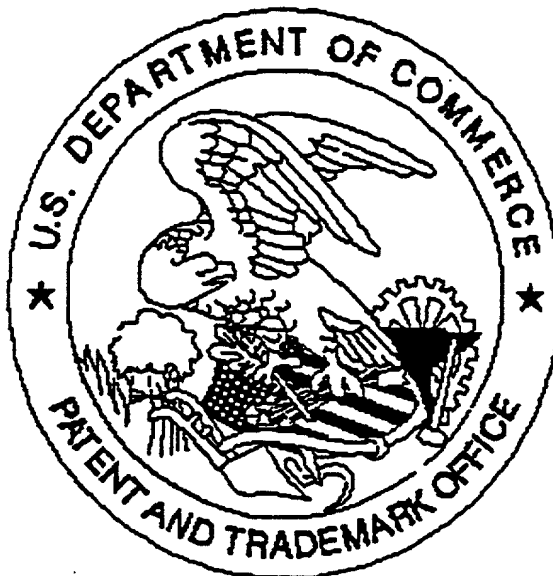
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Leu	Pro	His	Leu	His	Met	Asp	Val	Leu	Glu	Gly	Leu	Ile	Leu	Val	Leu
	-85					-80						-75			
Pro	Cys	Ile	Asp	Val	Phe	Val	Lys	Val	Asp	Leu	Arg	Thr	Val	Thr	Cys
-70					-65					-60					
Asn	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Arg	Asp	Ser	Val	Thr	Thr	Gln
-55				-50					-45						-40
Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Ile	Tyr	Ser	Ala	Val	Ser	Ala	Val
			-35					-30					-25		
Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe	Leu	Leu	Ala	Gln	Thr
	-20						-15					-10			
Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Gln	Thr	Leu	Ser	Gln	Ile	Leu	Ala
	-5					1				5					
Gly	Arg	Glu	Glu	Ile	Ala	His	Ser	Ile	Gln	Thr	Leu	Leu	Asp	Asp	Ala
10				15					20					25	
Thr	Glu	Leu	Trp	Gly	Ile	Arg	Val	Ala	Arg	Val	Glu	Ile	Lys	Asp	Val
			30					35					40		
Arg	Ile	Pro	Val	Gln	Leu	Gln	Arg	Ser	Met	Ala	Ala	Glu	Ala	Glu	Ala
		45					50					55			
Thr	Arg	Glu	Ala	Arg	Ala	Lys	Val	Leu	Ala	Ala	Glu	Gly	Glu	Met	Asn

		60					65				70						
Ala	Ser	Lys	Ser	Leu	Lys	Ser	Ala	Ser	Met	Val	Leu	Ala	Glu	Ser	Pro		
	75					80					85						
Ile	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	Gln	Thr	Leu	Ser	Thr	Val	Ala	Thr		
90					95					100					105		
Glu	Lys	Asn	Ser	Thr	Ile	Val	Phe	Pro	Leu	Pro	Met	Asn	Ile	Leu	Glu		
			110						115					120			
Gly	Ile	Gly	Gly	Val	Ser	Tyr	Asp	Asn	His	Lys	Lys	Leu	Pro	Asn	Lys		
			125					130					135				
Ala																	

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